Changed a file from non-ASCII to ASCII Changed the margins in cases where the sequence text was "wrapped" down to the life of the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an Changed the spelling of a mandatory field (the headings or subheadings), specifically: Inserted a space between the last nucleic designator and the nucleic number for sequences: Deleted page numbers in the text of the sequence listing, which is considered invalid text. Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited we inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa.	3/23/94
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A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.	
A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Other:	

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

8/01/93

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PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

TIME: 15:00:21

DATE: 03/23/94

1		SEQUENCE LISTING
2 3	(1) G	eneral Information:
4	(1)	
5 6 7 8 9	(i)	APPLICANT: Garner, Ian Dalrymple, Michael A Prunkard, Donna E Foster, Donald C
10 11	(ii)	TITLE OF INVENTION: Production of Fibrinogen in Transgenic Animals
12 13 14	(iii)	NUMBER OF SEQUENCES: 27
15 16 17 18 19 20 21	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: ZymoGenetics, Inc. (B) STREET: 4225 Roosevelt Way, N.E. (C) CITY: Seattle (D) STATE: WA (E) COUNTRY: USA (F) ZIP: 98105
22 23 24 25 26 27 28	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
29 30 31 32 33	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
34 35 36 37	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Parker, Gary E (B) REGISTRATION NUMBER: 31-648 (C) REFERENCE/DOCKET NUMBER: 93-15
38 39 40 41 42 43	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 206-547-8080 ext 322 (B) TELEFAX: 206-548-2329
44 45 46	(2) INFO	RMATION FOR SEQ ID NO:1:
47 48 49 50	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 5943 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

TIME: 15:00:27

DATE: 03/23/94

52 53 54 55	(ii) MOLECULE TYPE: DNA (genomic)	
56 57 58	<pre>(vii) IMMEDIATE SOURCE: (B) CLONE: Human Fibrinogen A-alpha chain</pre>	
59 60 61 62 63	<pre>(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: join(3184, 11541279, 17391922, 305532</pre>	200,
64 65 66	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
67 68 69 70	GTCTAGGAGC CAGCCCCACC CTTAGAAAAG ATG TTT TCC ATG AGG ATC GTC TGC Met Phe Ser Met Arg Ile Val Cys 1 5	54
71 72 73 74	CTA GTT CTA AGT GTG GTG GGC ACA GCA TGG GTATGGCCCT TTTCATTTTT Leu Val Leu Ser Val Val Gly Thr Ala Trp 10 15	104
75 76	TCTTCTTGCT TTCTCTCTGG TGTTTATTCC ACAAAGAGCC TGGAGGTCAG AGTCTACCTG	164
77 78	CTCTATGTCC TGACACACTC TTAGCTTTAT GACCCCAGGC CTGGGAGGAA ATTTCCTGGG	224
79 80	TGGGCTTGAC ACCTCAAGAA TACAGGGTAA TATGACACCA AGAGGAAGAT CTTAGATGGA	284
81 82	TGAGAGTGTA CAACTACAAG GGAAACTTTA GCATCTGTCA TTCAGTCTTA CCACATTTTG	344
83 84	TTTTGTTTTG TTTTAAAAAG GGCAAGAATT ATTTGCCATC CTTGTACCTA TAAAGCCTTG	404
85 86	GTGCATTATA ATGCTAGTTA ATGGAATAAA ACATTTTATG GTAAGATTTG TTTTCTTTAG	464
87 88	TTATTAATTT CTTGCTACTT GTCCATAATA AGCAGAACTT TTAGTGTTAG TACAGTTTTG	524
89	CTGAAAGGTT ATTGTTGTGT TTGTCAAGAC AGAAGAAAAA GCAAACGAAT TATCTTTGGA	584
90 91	AATATCTTTG CAGTATCAGA AGAGATTAGT TAGTAAGGCA ATACGCTTTT CCGCAGTAAT	644
92 93	GGTATTCTTT TAAATTATGA ATCCATCTCT AAAGGTTACA TAGAAACTTG AAGGAGAGAG	704
94 95	GAACATTCAG TTAAGATAGT CTAGGTTTTT CTACTGAAGC AGCAATTACA GGAGAAAGAG	764
96 97	CTCTACAGTA GTTTTCAACT TTCTGTCTGC AGTCATTAGT AAAAATGAAA AGGTAAAATT	824
98 99	TAACTGATTT TATAGATTCA AATAATTTTC CTTTTAGGAT GGATTCTTTA AAACTCCTAA	884
100 101 102	TATTTATCAA ATGCTTATTT AAGTGTCACA CACAGTTAAG AAATTTGTAC ACCTTGTCTC	944

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:00:32

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104	3.000033.000 M0000333.000 CM000000000 M000000033 M CM00000033 CM0000	
105 106	ACCTGAAGCT TGCCGAAGCC CTGTGTCTGC TCTCCTTAAT CTCTGTGAGA GTGCCATCTC	1064
107 108	TTCCTGGGGA CTTGTAGGCA TGCCACTGTC TCCTCTTCTG GCTAACATTG CTGTTGCTCT	1124
109	CTTTTGTGTA TGTGAATGAA TCTTTAAAG ACT GCA GAT AGT GGT GAA GGT GAC	1177
110	Thr Ala Asp Ser Gly Glu Gly Asp	,
111	20 25	
112		
113	TTT CTA GCT GAA GGA GGC GTG CGT GGC CCA AGG GTT GTG GAA AGA	1225
114	Phe Leu Ala Glu Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg	
115	30 35 40	
116		
117	CAT CAA TCT GCC TGC AAA GAT TCA GAC TGG CCC TTC TGC TCT GAT GAA	1273
118	His Gln Ser Ala Cys Lys Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu	
119	45 50 55	
120		
121	GAC TGG GTAAGCAGTC AGCGGGGGAA GCAGGAGATT CCTTCCCTCT GATGCTAGAG	1329
122	Asp Trp	
123	60	
124		
125	GGGCTCACAG GCTGACCTGA TTGGTCCCAG AAACTTTTTT AAATAGAAAA TAATTGAATA	1389
126		
127	GTTACCTACA TAGCAAATAA AGAAAAGGAA CCTACTCCCA AGAGCACTGT TTATTTACCT	1449
128		
129	CCCCAACTCT GGATCATTAG TGGGTGAACA GACAGGATTT CAGTTGCATG CTCAGGCAAA	1509
130		
131	ACCAGGCTCC TGAGTATTGT GGCCTCAATT TCCTGGCACC TATTTATGGC TAAGTGGACC	1569
132		
133	CTCATTCCAG AGTTTCTCTG CGACCTCTAA CTAGTCCTCT TACCTACTTT TAAGCCAACT	1629
134		
135 136	TATCTGGAAG AGAAAGGGTA GGAAGAAATG GGGGCTGCAT GGAAACATGC AAAATTATTC	1689
137	TGAATCTGAG AGATAGATCC TTACTGTAAT TTTCTCCCTT CACTTTCAG AAC TAC	1744
138	Asn Tyr	_ · - ·
139	/-	
140		
141	AAA TGC CCT TCT GGC TGC AGG ATG AAA GGG TTG ATT GAT GAA GTC AAT	1792
142	Lys Cys Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn	
143	65 70 75	
144		
145	CAA GAT TTT ACA AAC AGA ATA AAT AAG CTC AAA AAT TCA CTA TTT GAA	1840
146	Gln Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu	
147	80 85 90	
148		
149	TAT CAG AAG AAC AAT AAG GAT TCT CAT TCG TTG ACC ACT AAT ATA ATG	1888
150	Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met	
151	95 100 105 110	
152		
153	GAA ATT TTG AGA GGC GAT TTT TCC TCA GCC AAT A GTAAGTATTA	1932

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

TIME: 15:00:38

DATE: 03/23/94

154 155 156	Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn 115 120	
157 158	CATATTTACT TCTTTGACTT TATAACAGAA ACAACAAAAA TCCTAAATAA ATATGATATC	1992
159 160	CGCTTATATC TATGACAATT TCATCCCAAA GTACTTAGTG TAGAAACACA TACCTTCATA	2052
161 162	ATATCCCTGA AAATTTTAAG AGGGAGCTTT TGTTTTCGTT ATTTTTTCAA AGTAAAAGAT	2112
163 164	GTTAACTGAG ATTGTTTAAG GTCACAAAAT AAGTCAGAAT TTTGGATTAA AACAAGAATT	2172
165 166	TAAATGTGTT CTTTTCAACA GTATATACTG AAAGTAGGAT GGGTCAGACT CTTTGAGTTG	2232
167 168	ATATTTTTGT TTCTGCTTTG TAAAGGTGAA AACTGAGAGG TCAAGGAACT TGTTCAAAGA	2292
169 170	CACAGAGCTG GGAATTCAAC TCCCAGACTC CACTGAGCTG ATTAGGTAGA TTTTTAAATT	2352
171 172	TAAAATATAG GGTCAAGCTA CGTCATTCTC ACAGTCTACT CATTAGGGTT AGGAAACATT	2412
173 174	GCATTCACTC TGGGCATGGA CAGCGAGTCT AGGGAGTCCT CAGTTTCTCA AGTTTTGCTT	2472
175 176	TGCCTTTTTA CACCTTCACA AACACTTGAC ATTTAAAATC AGTGATGCCA ACACTAGCTG	2532
177 178	GCAAGTGAGT GATCCTGTTG ACCCAAAACA GCTTAGGAAC CATTTCAAAT CTATAGAGTT	2592
179 180 181	AAAAAGAAAA GCTCATCAGT AAGAAAATCC AATATGTTCA AGTCCCTTGA TTAAGGATGT TATAAAATAA TTGAAATGCA ATCAAACCAA CTATTTTAAC TCCAAATTAC ACCTTTAAAA	2652 2712
182 183	TTCCAAAGAA AGTTCTTCTT CTATATTTCT TTGGGATTAC TAATTGCTAT TAGGACATCT	2712
184 185	TAACTGGCAT TCATGGAAGG CTGCAGGGCA TAACATTATC CAAAAGTCAA ATGCCCCATA	2832
186 187	GGTTTTGAAC TCACAGATTA AACTGTAACC AAAATAAAAT	2892
188 189	TTTCTTTCTT TCTTTTTCT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT	2952
190 191	CTTTCTTTCT TTCTCCTTCC TTCCTTTCTT CCTTTCTTT TTGCTGGCAA TTACAGACAA	3012
192 193 194 195 196	ATCACTCAGC AGCTACTTCA ATAACCATAT TTTCGATTTC AG AC CGT GAT AAT Asn Arg Asp Asn 125	3065
197 198 199 200	ACC TAC AAC CGA GTG TCA GAG GAT CTG AGA AGC AGA ATT GAA GTC CTG Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu 130 135 140	3113
201 202 203 204	AAG CGC AAA GTC ATA GAA AAA GTA CAG CAT ATC CAG CTT CTG CAG AAA Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys 145 150 155	3161

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

TIME: 15:00:43

DATE: 03/23/94

205 206 207 208	AAT GTT AGA GCT CAG TTG GTT GAT ATG AAA CGA CTG GAG GTAAGTATGT Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu Glu 160 165 170	3210
209 210	GGCTGTGGTC CCGAGTGTCC TTGTTTTTGA GTAGAGGGAA AAGGAAGGCG ATAGTTATGC	3270
211 212	ACTGAGTGTC TACTATATGC AGAGAAAAGT GTTATATCCA TCATCTACCT AAAAGTAGGT	3330
213 214	ATTATTTTCC TCACTCCACA GTTGAAGAAA AAAAAATTCA GAGATATTAA GTAAATTTTC	3390
215 216	CAACGTACAT AGATAGTAAT TCAAAGCAAT GTTCAGTCCC TGTCTATTCC AAGCCATTAC	3450
217 218	ATCACCACAC CTCTGAGCCC TCAGCCTGAG TTCACCAAGG ATCATTTAAT TAGCGTTTCC	3510
219 220	TTTGAGAGGG AATAGCACCT TACTCTTGAT CCATTCTGAG GCTAAGATGA ATTAAACAGC	3570
221	ATCCATTGCT TATCCTGGCT AGCCCTGCAA TACCCAACAT CTCTTCCACT GAGGGTGCTC	3630
223 224	GATAGGCAGA AAACAGAGAA TATTAAGTGG TAGGTCTCCG AGTCAAAAAA AATGAAACCA	3690
225 226	GTTTCCAGAA GGAAAATTAA CTACCAGGAA CTCAATAGAC GTAGTTTATG TATTTGTATC	3750
227 228 229 230	TACATTTTCT CTTTATTTTT CTCCCCTCTC TCTAG GTG GAC ATT GAT ATT AAG Val Asp Ile Asp Ile Lys 175	3803
231 232 233 234	ATC CGA TCT TGT CGA GGG TCA TGC AGT AGG GCT TTA GCT CGT GAA GTA Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val 180 185 190	3851
235 236 237 238	GAT CTG AAG GAC TAT GAA GAT CAG CAG AAG CAA CTT GAA CAG GTC ATT Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys Gln Leu Glu Gln Val Ile 195 200 205	3899
239 240 241 242	GCC AAA GAC TTA CTT CCC TCT AGA GAT AGG CAA CAC TTA CCA CTG ATA Ala Lys Asp Leu Leu Pro Ser Arg Asp Arg Gln His Leu Pro Leu Ile 210 215 220	3947
243 244 245 246	AAA ATG AAA CCA GTT CCA GAC TTG GTT CCC GGA AAT TTT AAG AGC CAG Lys Met Lys Pro Val Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln 230 235 240	3995
247 248 249 250	CTT CAG AAG GTA CCC CCA GAG TGG AAG GCA TTA ACA GAC ATG CCG CAG Leu Gln Lys Val Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln 245 250 255	4043
251 252 253 254	ATG AGA ATG GAG TTA GAG AGA CCT GGT GGA AAT GAG ATT ACT CGA GGA Met Arg Met Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly 260 265 270	4091
255	GGC TCC ACC TCT TAT GGA ACC GGA TCA GAG ACG GAA AGC CCC AGG AAC	4139

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

TIME: 15:00:48

DATE: 03/23/94

256 257 258	Gly	Ser	Thr 275	Ser	Tyr	Gly	Thr	Gly 280	Ser	Glu	Thr	Glu	Ser 285	Pro	Arg	Asn	
259 260 261 262						AGC Ser											4187
263 264 265 266						CCT Pro 310											4235
267 268 269 270						TCT Ser											4283
271 272 273 274						GGA Gly											4331
275 276 277 278						GGA Gly											4379
279 280 281 282						ACC Thr											4427
283 284 285 286						TCT Ser 390											4475
287 288 289 290						AAC Asn											4523
291 292 293 294						CCA Pro											4571
295 296 297 298						GGA Gly											4619
299 300 301 302						ACA Thr											4667
303 304 305 306						ATT Ile 470											4715

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:00:53

307	GAA	GTG	GTG	ACC	TCC	GAA	GAT	GGT	TCT	GAC	TGT	CCC	GAG	GCA	ATG	GAT	4763
308	Glu	Val	Val	Thr	Ser	Glu	Asp	Gly	Ser	Asp	Cys	Pro	Glu	Ala	Met	Asp	
309					485					490					495		
310																	
311					TCT												4811
312	Leu	Gly	Thr		Ser	Gly	Ile	Gly		Leu	Asp	Gly	Phe	Arg	His	Arg	
313				500					505					510			
314																	
315					GCT												4859
316	His	Pro		Glu	Ala	Ala	Phe		Asp	Thr	Ala	Ser		Gly	Lys	Thr	
317			515					520					525				
318	mma	007	aam	mma.	mma	max	0.CM	3 mg		~~~	a. a		ama	3.00	~~~	3. GM	4005
319																ACT	4907
320	Pne		GIY	Pne	Phe	ser		мес	ьeu	GIĀ	GIU		vai	ser	GIU	Thr	
321 322		530					535					540					
323	CAC	TOT.	אממ	aaa	TCA	C 7 7	тст	ccc	አጥሮ	TTTC	א מיא	ייי ע ע	א מיז	7 7 C	C 7 7	TCC	4955
323					Ser												4333
325	545	Ser	Arg	дту	Ser	550	261	GIY	116	FIIC	555	ASII	1111	цуъ	GIU	560	
326	243					330					333					300	
327	AGT	ጥርጥ	САТ	CAC	CCT	GGG	ΔΤΔ	GCT	GAA	ጥጥር	ССТ	יי תיכי	ССТ	GGT	ΔΔΔ	тст	5003
328					Pro												5005
329					565	1				570			5	U -1	575	202	
330																	
331	TCA	AGT	TAC	AGC	AAA	CAA	TTT	ACT	AGT	AGC	ACG	AGT	TAC	AAC	AGA	GGA	5051
332	Ser	Ser	Tyr	Ser	Lys	Gln	Phe	Thr	Ser	Ser	Thr	Ser	Tyr	Asn	Arg	Gly	
333			-	580	-				585				•	590	•	-	
334																	
335	GAC	TCC	ACA	TTT	GAA	AGC	AAG	AGC	TAT	AAA	ATG	GCA	GAT	GAG	GCC	GGA	5099
336	Asp	Ser	Thr	Phe	Glu	Ser	Lys	Ser	Tyr	Lys	Met	Ala	Asp	Glu	Ala	Gly	
337			595					600					605				
338																	
339					CAT												5147
340	Ser		Ala	Asp	His	Glu		Thr	His	Ser	Thr		Arg	Gly	His	Ala	
341		610					615					620					
342		mam	~~~	aam	ama		~~~		~~~			aam		~~~			5105
343					GTC												5195
344		ser	arg	Pro	Val		GIĀ	me	HIS	Thr		Pro	ьeu	GIA	ьys		
345 346	625					630					635					640	
347	יייכיכ	СТС	TCC	מממ	TAGA	ላ ርተጥ አ ን	\ ረ ሞ ፣	יא <i>א</i> אי	וי א יחיחינ	ירי ידינ	ברוא רו	א כשיכי	י ייירינ	ግር አጥር	במממ		5247
348		Leu			IAG	CIM	1 G1 .	IAAA.	IAII.		JCAC	AG 1 G .	1 10	CAI	3000		3241
349	Der	пси	DCI	110	645												
350					013												
351	CCT	rgca'	rtt (CCTT	CTTA	AC TO	СТСТС	GTTAC	C ACC	TCA	TTGA	AAC	raca(CTT	rttt	GTCTG	5307
352																	
353	TTT	TTGT	GCT A	AGAC	rgta <i>i</i>	AG T	rcct'	rggg	G GC	AGGG	CCTT	TGT	CTGT	CTC Z	ATCT	CTGTAT	5367
354																	
355	TCC	CAAA'	rgc (CTAA	CAGT	AC AC	BAGC	CATG	A CT	CAAT	TAAA	ACA!	rgtt	AAA :	rgga'	rgaatg	5427
356																	
357	AAT	rcct(CTG A	AAAC'	rcta:	TT TO	GAGC'	TAT:	TAC	STCA/	TTAA	CTT'	rcac'	TAT	rcaa.	AGTGTG	5487

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2 = 2																	
358																	
359	TGCT	ATTA(SA A	TTGT	CAC	CC A	ACTG	ATTA	A TC	ACAT	$\Gamma T T T$	AGT	TGT	STC 7	rcag'	TGAC	A 5547
360																	
361	TTTAC	GGTC	AG G	CTA	ATAC	CA AC	GTTG:	rgtt <i>f</i>	A GT	ATTA	AGTG	AGC	TAG	CTA (CCTGT	ACTG	G 5607
362																	,
363	TTACT	TTGC:	ra i	TAG	rttg:	rg C	AAGT?	LAAA	TCC	CAAA	raca	TTTC	BAGG	AAA	ATCC	CTTT	G 5667
364																	
365	CAATT	TTGT?	AG G	TAT	LAAT	AA C	CGCT:	TTTA1	GC	AATAA(FTTC	TATO	CCAC	TG T	[AAG]	GCAT	C 5727
366																	
367	CTTTC	CCCT	AT G	GAGG	GAAC	G A	AAGG?	AGGAZ	A GAZ	\AGA/	AAGG	AAGO	GAA	AGA A	AACAG	TTATE	T 5787
368																	
369	GCCTT	TATT:	ra a	TCTC	BAGCO	CG TO	GCT?	ATCT1	TG?	DAAAT	ATTE	AATO	AGA	ATA A	ACTTO	TTCC	A 5847
370																	
371	ACCAC	GCTT?	I AA	TTTT	CTTTT	T A	JACT(TGA T	GA'	rgtco	CTCC	AAA	'ACA'	rcc 1	TCAC	GTAC	C 5907
372																	
373	CAAAC	GTGG	CA I	TTTC	CAATA	AT C	AAGC:	CATCO	GGZ	ATCC							5943
374																	
375																	
376	(2)	INFO	RMAT	'ION	FOR	SEQ	ID 1	NO:2:									
377	• •					~											
378		(:	i) S	EQUE	ENCE	CHAI	RACTI	ERIST	CICS	:							
379		·	•	_				ami			3						
380								aci									
381				(D)	TOP	OLO	GY:]	linea	ir								
382				, - ,													
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384																	
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385		(x:					•	rion:		O ID	NO:2	2:					
385 386	Met I		i) S	EQUE	ENCE	DES	CRIP	rion:	SEÇ	•			Val	Val	Glv	Thr	
385 386 387	Met I		i) S	EQUE	ENCE Arg	DES	CRIP	rion:	SEÇ	Val			Val	Val	_	Thr	
385 386 387 388	Met I		i) S	EQUE	ENCE	DES	CRIP	rion:	SEÇ	•			Val	Val	Gly 15	Thr	
385 386 387 388 389	1	Phe S	i) S Ser	EQUE Met	ENCE Arg 5	DESO	CRIP	rion: Cys	: SE(Val 10	Leu	Ser			15		
385 386 387 388 389 390		Phe S	i) S Ser	EQUE Met Ala	ENCE Arg 5	DESO	CRIP	rion: Cys	SE(Leu Gly	Val 10	Leu	Ser		Glu	15		
385 386 387 388 389 390 391	1	Phe S	i) S Ser	EQUE Met	ENCE Arg 5	DESO	CRIP	rion: Cys	: SE(Val 10	Leu	Ser			15		
385 386 387 388 389 390 391 392	1 Ala 1	Phe s	i) S Ser Thr	EQUE Met Ala 20	Arg 5 Asp	DESC Ile Ser	CRIPT Val Gly	rion: Cys Glu	Leu Gly 25	Val 10 Asp	Leu Phe	Ser Leu	Ala	Glu 30	15 Gly	Gly	
385 386 387 388 389 390 391 392 393	1	Phe s	i) S Ser Thr Arg	EQUE Met Ala 20	Arg 5 Asp	DESC Ile Ser	CRIPT Val Gly	FION: Cys Glu Val	Leu Gly 25	Val 10 Asp	Leu Phe	Ser Leu	Ala Ser	Glu 30	15 Gly	Gly	
385 386 387 388 389 390 391 392 393 394	1 Ala 1	Phe s	i) S Ser Thr	EQUE Met Ala 20	Arg 5 Asp	DESC Ile Ser	CRIPT Val Gly	rion: Cys Glu	Leu Gly 25	Val 10 Asp	Leu Phe	Ser Leu	Ala	Glu 30	15 Gly	Gly	
385 386 387 388 389 390 391 392 393 394 395	1 Ala 1 Gly V	Phe S	i) Ser Thr Arg 35	Met Ala 20 Gly	Arg 5 Asp Pro	DESC Ile Ser Arg	CRIPT Val Gly Val	Cys Glu Val 40	Leu Gly 25 Glu	Val 10 Asp	Leu Phe His	Ser Leu Gln	Ala Ser 45	Glu 30 Ala	15 Gly Cys	Gly Lys	
385 386 387 388 389 390 391 392 393 394 395 396	1 Ala 1	Phe STrp Twal A	i) Ser Thr Arg 35	Met Ala 20 Gly	Arg 5 Asp Pro	DESC Ile Ser Arg	Val Cys	Cys Glu Val 40	Leu Gly 25 Glu	Val 10 Asp	Leu Phe His	Ser Leu Gln Trp	Ala Ser 45	Glu 30 Ala	15 Gly Cys	Gly Lys	
385 386 387 388 389 390 391 392 393 394 395 396 397	1 Ala 1 Gly V	Phe S	i) Ser Thr Arg 35	Met Ala 20 Gly	Arg 5 Asp Pro	DESC Ile Ser Arg	CRIPT Val Gly Val	Cys Glu Val 40	Leu Gly 25 Glu	Val 10 Asp	Leu Phe His	Ser Leu Gln	Ala Ser 45	Glu 30 Ala	15 Gly Cys	Gly Lys	
385 386 387 388 389 390 391 392 393 394 395 396 397 398	Ala T	Phe S Trp 5 Val 1 Ser 1	i) Ser Thr Arg 35	Met Ala 20 Gly Trp	Arg 5 Asp Pro	DESC Ile Ser Arg	CRIPT Val Gly Val Cys 55	Cys Glu Val 40 Ser	Gly 25 Glu Asp	Val 10 Asp Arg	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn	Glu 30 Ala Tyr	15 Gly Cys Lys	Gly Lys Cys	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399	Ala Caly Value Asp S	Phe S Trp 5 Val 1 Ser 1	i) Ser Thr Arg 35	Met Ala 20 Gly Trp	Arg 5 Asp Pro	DESC Ile Ser Arg Phe	CRIPT Val Gly Val Cys 55	Cys Glu Val 40 Ser	Gly 25 Glu Asp	Val 10 Asp Arg	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn	Glu 30 Ala Tyr	15 Gly Cys Lys	Gly Lys Cys Asp	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400	Ala T	Phe S Trp 5 Val 1 Ser 1	i) Ser Thr Arg 35	Met Ala 20 Gly Trp	Arg 5 Asp Pro	DESC Ile Ser Arg	CRIPT Val Gly Val Cys 55	Cys Glu Val 40 Ser	Gly 25 Glu Asp	Val 10 Asp Arg	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn	Glu 30 Ala Tyr	15 Gly Cys Lys	Gly Lys Cys	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401	Ala Cally Name of the	Phe S Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp	Arg 5 Asp Pro Pro	DESC Ile Ser Arg Phe Met	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser	Leu Gly 25 Glu Asp	Val 10 Asp Arg Glu	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn	15 Gly Cys Lys Gln	Gly Lys Cys Asp	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402	Ala Caly Value Asp S	Phe S Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp	Arg 5 Asp Pro Pro Arg	DESC Ile Ser Arg Phe Met	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser	Leu Gly 25 Glu Asp	Val 10 Asp Arg Glu Ile	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn	Gly Cys Lys Gln Tyr	Gly Lys Cys Asp	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403	Ala Cally Name of the	Phe S Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp	Arg 5 Asp Pro Pro	DESC Ile Ser Arg Phe Met	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser	Leu Gly 25 Glu Asp	Val 10 Asp Arg Glu	Leu Phe His Asp	Ser Leu Gln Trp 60	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn	15 Gly Cys Lys Gln	Gly Lys Cys Asp	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404	Ala Caly Value Asp San	Phe S Trp T Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp Cys	Arg 5 Asp Pro Pro Arg 11e 85	DESC Ile Ser Arg Phe Met 70	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser Gly Leu	Leu Gly 25 Glu Asp Leu Lys	Val 10 Asp Arg Glu Ile Asn 90	Leu Phe His Asp 75 Ser	Ser Leu Gln Trp 60 Glu Leu	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn Glu	15 Gly Cys Lys Gln Tyr 95	Gly Lys Cys Asp 80 Gln	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405	Ala Cally Name of the	Phe S Trp T Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp Cys Arg	Arg 5 Asp Pro Pro Arg 11e 85	DESC Ile Ser Arg Phe Met 70	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser Gly Leu	Leu Gly 25 Glu Asp Leu Lys	Val 10 Asp Arg Glu Ile Asn 90	Leu Phe His Asp 75 Ser	Ser Leu Gln Trp 60 Glu Leu	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn Glu Met	15 Gly Cys Lys Gln Tyr 95	Gly Lys Cys Asp 80 Gln	
385 386 387 388 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406	Ala Caly Value Asp San	Phe S Trp T Val 1 Ser 1 Ser (i) Ser Thr Arg 35 Asp	EQUE Met Ala 20 Gly Trp Cys	Arg 5 Asp Pro Pro Arg 11e 85	DESC Ile Ser Arg Phe Met 70	CRIPT Val Gly Val Cys 55 Lys	Cys Glu Val 40 Ser Gly Leu	Leu Gly 25 Glu Asp Leu Lys	Val 10 Asp Arg Glu Ile Asn 90	Leu Phe His Asp 75 Ser	Ser Leu Gln Trp 60 Glu Leu	Ala Ser 45 Asn Val	Glu 30 Ala Tyr Asn Glu	15 Gly Cys Lys Gln Tyr 95	Gly Lys Cys Asp 80 Gln	
385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405	Ala Caly Value Asp San	Phe S Trp T Val 1 Ser 1 Ser (Thr 1 Asn 1	i) Ser Thr Arg 35 Asp Gly Asn	EQUE Met Ala 20 Gly Trp Cys Arg	Arg Asp Pro Pro Arg Ile 85 Asp	DESC Ile Ser Arg Phe Met 70 Asn	CRIPT Val Gly Val Cys 55 Lys Lys	Cys Glu Val 40 Ser Gly Leu Ser	Leu Gly 25 Glu Asp Leu Lys Leu 105	Val 10 Asp Arg Glu Ile Asn 90 Thr	Leu Phe His Asp 75 Ser	Ser Leu Gln Trp 60 Glu Leu Asn	Ala Ser 45 Asn Val Phe	Glu 30 Ala Tyr Asn Glu Met 110	Gly Cys Lys Gln Tyr 95	Gly Lys Cys Asp 80 Gln	

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409			115					120					125			
410	_		_	~-3	_	_	_	_	_				_	_	_	_
411 412	Arg	130	ser	GIU	Asp	ьeu	Arg	ser	Arg	ше	GIu		Leu	Lys	Arg	Lys
413		130					133					140				
414	Val	Ile	Glu	Lvs	Val	Gln	His	Ile	Gln	Leu	Leu	Gln	Lvs	Asn	Val	Ara
415	145			-1-		150					155		-1-			160
416																
417	Ala	Gln	Leu	Val	Asp	Met	Lys	Arg	Leu	Glu	Val	Asp	Ile	Asp	Ile	Lys `
418					165					170					175	
419																
420	Ile	Arg	Ser	-	Arg	Gly	Ser	Cys		Arg	Ala	Leu	Ala	_	Glu	Val
421				180					185					190		
422	7	T	T	7		~1	7	~1	a1	T	~1	T	a 1	~1	77-3	T1 -
423 424	Asp	ьeu	ьуs 195	Asp	Tyr	GIU	Asp	200	GIN	гÀг	GIN	Leu		GIN	Val	TTE
425			193					200					205			
426	Δla	Lvs	Asn	Leu	Len	Pro	Ser	Ara	Asp	Ara	Gln	His	T.e.i	Pro	Leu	Tle
427	1114	210	тър	Lou	204		215		пор	9	Q1	220	u	110		
428																
429	Lys	Met	Lys	Pro	Val	Pro	Asp	Leu	Val	Pro	Gly	Asn	Phe	Lys	Ser	Gln
430	225		-			230	_				235			_		240
431																
432	Leu	Gln	Lys	Val		Pro	Glu	\mathtt{Trp}	Lys		Leu	Thr	Asp	Met	Pro	${\tt Gln}$
433					245					250					255	
434		_		~3	_	~7	_	_		~7	_	~-7		_,	_	
435	Met	Arg	Met		Leu	GIu	Arg	Pro	_	GIY	Asn	GIu	шe		Arg	GLY
436 437				260					265					270		
437	Glv	Ser	Thr	Ser	ጥህዮ	G] v	Thr	G1 v	Ser	G111	Thr	G111	Ser	Dro	Arg	Λen
439	CLY	DCI	275	DCI	- 7 -	GLY	1111	280	DCI	OLU	1111	OIu	285	110	nr 9	ASII
440			,					200								
441	Pro	Ser	Ser	Ala	Gly	Ser	Trp	Asn	Ser	Gly	Ser	Ser	Gly	Pro	Gly	Ser
442		290			•		295			•		300	•		•	
443																
444		Gly	Asn	Arg	Asn		Gly	Ser	Ser	Gly	Thr	Gly	Gly	Thr	Ala	Thr
445	305					310					315					320
446	M	T	D	a 1	G	a	a 1	D	~1	a	77 -	a 1	0		3	a
447 448	Trp	ьуs	Pro	GIA	325	ser	GIA	Pro	GIY	330	АТА	GIY	ser	Trp	Asn 335	ser
449					323					330					333	
450	Glv	Ser	Ser	Glv	Thr	Glv	Ser	Thr	Glv	Asn	Gln	Asn	Pro	Glv	Ser	Pro
451	0-1			340		1			345					350		
452								•								
453	Arg	Pro	Gly	Ser	Thr	Gly	Thr	Trp	Asn	Pro	Gly	Ser	Ser	Glu	Arg	Gly
454			355			-		360			-		365		-	_
455		_														
456	Ser		Gly	His	\mathtt{Trp}	Thr		Glu	Ser	Ser	Val		Gly	Ser	Thr	Gly
457		370					375					380				
458	71 -	TT 7070	TT -2 ~	C	01.	C ~ ~	a 1	0	Db-	7	Dres	7	0	Dese	a 1	C a
459	GIN	Trp	HIS	ser	GLU	ser	GTĀ	ser	rne	arg	Pro	Asp	ser	Pro	GТĀ	Ser

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460 461	385					390					395					400
462 463 464	Gly	Asn	Ala	Arg	Pro 405	Asn	Asn	Pro	Asp	Trp 410	Gly	Thr	Phe	Glu	Glu 415	Val
465 466 467	Ser	Gly	Asn	Val 420	Ser	Pro	Gly	Thr	Arg 425	Arg	Glu	Tyr	His	Thr 430	Glu	Lys
468 469 470	Leu	Val	Thr 435	Ser	Lys	Gly	Asp	Lys 440	Glu	Leu	Arg	Thr	Gly 445	_	Glu	Lys
471 472 473	Val	Thr 450	Ser	Gly	Ser	Thr	Thr 455	Thr	Thr	Arg	Arg	Ser 460	Cys	Ser	Lys	Thr
474 475 476	Val '465	Thr	Lys	Thr	Val	Ile 470	Gly	Pro	Asp	Gly	His 475	Lys	Glu	Val	Thr	Lys 480
477 478 479	Glu	Val	Val	Thr	Ser 485	Glu	Asp	Gly	Ser	Asp 490	Cys	Pro	Glu	Ala	Met 495	Asp
480 481 482	Leu	Gly	Thr	Leu 500	Ser	Gly	Ile	Gly	Thr 505	Leu	Asp	Gly	Phe	Arg 510	His	Arg
483 484 485	His	Pro	Asp 515	Glu	Ala	Ala	Phe	Phe 520	Asp	Thr	Ala	Ser	Thr 525	Gly	Lys	Thr
486 487 488	Phe	Pro 530	Gly	Phe	Phe	Ser	Pro 535	Met	Leu	Gly	Glu	Phe 540	Val	Ser	Glu	Thr
489 490 491	Glu 545	Ser	Arg	Gly	Ser	Glu 550	Ser	Gly	Ile	Phe	Thr 555	Asn	Thr	Lys	Glu	Ser 560
492 493 494	Ser	Ser	His	His	Pro 565	Gly	Ile	Ala	Glu	Phe 570	Pro	Ser	Arg	Gly	Lys 575	Ser
495 496 497	Ser	Ser	Tyr	Ser 580	Lys	Gln	Phe	Thr	Ser 585	Ser	Thr	Ser	Tyr	Asn 590	Arg	Gly
498 499 500	Asp	Ser	Thr 595	Phe	Glu	Ser	Lys	Ser 600	Tyr	Lys	Met	Ala	Asp 605	Glu	Ala	Gly
501 502 503	Ser	Glu 610	Ala	Asp	His	Glu	Gly 615	Thr	His	Ser	Thr	Lys 620	Arg	Gly	His	Ala
504 505 506	Lys 625	Ser	Arg	Pro	Val	Arg 630	Gly	Ile	His	Thr	Ser 635	Pro	Leu	Gly	Lys	Pro 640
507 508 509	Ser	Leu	Ser	Pro												
510	(2)	INF	ORMA!	rion	FOR	SEQ	ID I	NO:3	:							

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511			
512	(1)	EQUENCE CHARACTE	
513		(A) LENGTH: 8878	
514		(B) TYPE: nuclei	
515		(C) STRANDEDNESS	
516		(D) TOPOLOGY: li	near
517			
518	(ii)	OLECULE TYPE: DN	MA (genomic)
519			
520			
521	(vii)	MMEDIATE SOURCE:	
522	,		fibrinogen B-beta chain
523		(2, 020121 1141141	. I I I I I I I I I I I I I I I I I I I
524	(iv)	EATURE:	
525	((A) NAME/KEY: mi	ec PNA
526		(B) LOCATION: 1.	
527		(B) LOCATION: 1.	.403
528	(125)	EATURE:	·
529	(TX)		
530		<pre>(A) NAME/KEY: ex (B) LOCATION: 47</pre>	
		(B) LOCATION: 47	0583
531	(2)		
532	(1X)	EATURE:	4
533		(A) NAME/KEY: in	
534		(B) LOCATION: 58	43257
535			
536	(1X)	EATURE:	
537		(A) NAME/KEY: ex	
538		(B) LOCATION: 32	583449
539			
540	(ix)	EATURE:	
541		(A) NAME/KEY: in	tron
542		(B) LOCATION: 34	503938
543			
544	(ix)	EATURE:	
545		(A) NAME/KEY: ex	on
546		(B) LOCATION: 39	394122
547			
548	(ix)	EATURE:	
549		(A) NAME/KEY: in	tron
550		(B) LOCATION: 41	.235042
551			
552	(ix)	EATURE:	
553		(A) NAME/KEY: ex	con
554		(B) LOCATION: 50	
555		,	
556	(ix)	'EATURE :	
557	,,	(A) NAME/KEY: in	tron
558		(B) LOCATION: 52	
559		,_,	
560	(ix)	EATURE:	
561	,	(A) NAME/KEY: ex	on .
		,	

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562	(B)	LOCATION:	5831594	14			
563							
564	(ix) FEAT						
565		NAME/KEY:					
566	(B)	LOCATION:	5945663	32			
567							
568	(ix) FEAT	URE:					
569	(A)	NAME/KEY:	exon				
570	(B)	LOCATION:	6633675	58			
571							
572	(ix) FEAT	URE:					
573	(A)	NAME/KEY:	intron				
574	(B)	LOCATION:	6759696	66 ·			
575							
576	(ix) FEAT	TURE:					
577	(A)	NAME/KEY:	exon				
578		LOCATION:		52			
579	(-,			_			
580	(ix) FEAT	TIRE:					
581	, ,	NAME/KEY:	intron				
582		LOCATION:		7.0			
583	(1)	DOCALION.	723370	. •			
584							
585	(ix) FEAT	गार्क :					
586	• •	NAME/KEY:	AVOD				
587		LOCATION:		12			
588	(B)	LOCATION:	/6/1610	02			
	/dea) 1717 7	orm a					
589	(ix) FEAT		2 / 11000				
590		NAME/KEY:		. =			
591	(B)	LOCATION:	8103853	3.7			
592	()						
593	(ix) FEAT						
594		NAME/KEY:	_				
595	(B)	LOCATION:	8538887	78			
596							
597	(ix) FEAT						
598		NAME/KEY:					
599	(B)	LOCATION:	join(470.	583, 3258	3449, 3939	94122, 504	35270,
600		58315	5944, 6633	36758, 69	677252, 78	8718102)	
601							
602							
603	(xi) SEQU	JENCE DESCRI	IPTION: SE	EQ ID NO:3:			
604							
605	GAATTCATGC CO	CTTTTGAA AT	FAGACTTAT	GTCATTGTCA	GAAAACATAA	GCATTTATGG	60
606							
607	TATATCATTA AT	GAGTCACG AT	TTTTAGTGG	TTGCCTTGTG	AGTAGGTCAA	ATTTACTAAG	120
608							
609	CTTAGATTTG TT	TTCTCACA T	ATTCTTTCG	GAGCTTGTGT	AGTTTCCACA	TTAATTTACC	180
610							
611	AGAAACAAGA TA	ACACACTCT C	TTGAGGAG	TGCCCTAACT	TCCCATCATT	TTGTCCAATT	240
612							
				•			

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613 614	AAATGAATTG AAGAAATTTA ATGTTTCTAA ACTAGACCAA CAAAGAATAA TAGTTGTATG	300
615	ACAAGTAAAT AAGCTTTGCT GGGAAGATGT TGCTTAAATG ATAAAATGGT TCAGCCAACA	360
616 617	AGTGAACCAA AAATTAAATA TTAACTAAGG AAAGGTAACC ATTTCTGAAG TCATTCCTAG	420
618 619 620 621	CAGAGGACTC AGATATATAT AGGATTGAAG ATCTCTCAGT TAAGTCTAC ATG AAA Met Lys	475
622 623 624 625	AGG ATG GTT TCT TGG AGC TTC CAC AAA CTT AAA ACC ATG AAA CAT CTA Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys His Leu 5 10 15	523
626 627 628 629	TTA TTG CTA CTA TTG TGT GTT TTT CTA GTT AAG TCC CAA GGT GTC AAC Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly Val Asn 20 25 30	571
630 631 632 633	GAC AAT GAG GAG GTGAATTTTT TAAAGCATTA TTATATTATT AGTAGTATTA Asp Asn Glu Glu 35	623
634 635 636	TTAATATAAG ATGTAACATA ATCATATTAT GTGCTTATTT TAATGAAATT AGCATTGCTT	683
637	ATAGTTATGA AATGGAATTG TTAACCTCTG ACTTATTGTA TTTAAAGAAT GTTTCATAGT	743
638 639	ATTTCTTATA TAAAAACAAA GTAATTTCTT GTTTTCTAGT TTATCACCTT TGTTTTCTTA	803
640 641	AGATGAGGAT GGCTTAGCTA ATGTAAGATG TGTTTTTCTC ACTTGCTATT CTGAGTACTG	863
642 643	TGATTTTCAT TTACTTCTAG CAATACAGGA TTACAATTAA GAGGACAAGA TCTGAAAATC	923
644 645	TCACAAACTA TAAAATAATA AAAGAGCAGA ATTTTAAGAT AAAAGAAACT GGTGGTAGGT	983
646 647 648	AGATTGTTCT TTGGTGAAGG AAGGTAATAT ATATTGTTAC TGAGATTACT ATTTATAAAA	1043
649 650	ATTATAACTA AGCCTAAAAG CAAAATACAT CAAGTGTAAT GATAGAAAAT GAAATATTGC	1103
651 652	TTTTTTCAGA TGAAAAGTTC AAATTAGAGT TAGTGTGTAT TGTTATTATT AATAGTTATG	1163
653	AAACACGGTT CAGTCTAATT TATTTATTTG TAGAACAGTT TGTCCTCAAC TATTATTTTT	1223
654 655	GCTGACTTAT TGCTGTTAAT TTGCAGTTAC TAAAAATACA GAAATGCATT TAGGACAATG	1283
656 657	GATATTTAAG AAATTTAAAT TTTATCATCA AACGTATCAT GGCCAAATTT CTTACATATA	1343
658 659	GCATAGTATC ATTAAACTAG AAATAAGAAT ACACAATAAT ATTTAAATGA AGTGATTCAT	1403
660 661	TTCGGATCAT TATTGAGTTT CAAGGGAACT TGAGTGTTGT ACTTATCAGA CTCTACATGT	1463
662 663	AAGAACATAT AGTTAATCTG GTTGTGTGT TAAAAACATA TGGTTAATCT GGTTAAGTCT	1523

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664							
665	GGTTAATCAT	ATTAGGTAAG	AAAAATGTAA	AGAATGTGTA	AGACGAAATT	TTTGTAAAGT	1583
666							
667	ACTCTGCAAA	GCACTTTCAC	ATTTCTGCTT	ATCAACTAAA	CCTCACAGAG	ATAGTTTAAT	1643
668 669	AGTTTAGGCT	TTAAAATGGA	ጥጥጥ ሮልጥጥልጥ	тсаасаастс	GCCTTCATAA	ጥጥርጥጥጥል ል ር፥	1703
670		1111111110011		10.110.110.10	00011011111	11101111110	1,03
671	TGTTTTTCTT	TAAGTATATA	CTTTCTTTAA	$\mathbf{ATATTTTTA}$	AAATTTCCTT	TTCTCTAGTA	1763
672		3 maa3 maam3	COMOMOMA OM	2222 CTCTC2			
673 674	AAGCCAGACC	ATCCATGCTA	CCTCTCTAGT	GGCACTCTGA	AATAAAAAGA	AAATAGTTTT	1823
675	CTCTGTTATA	ATTGTATTTG	TAATAAGCAG	ATGAATCACA	TTTCTTAAAA	TTTGTTTTAG	1883
676							
677	AGAGGGTAAG	CTCTGACTAG	GACCATGACT	TCAATGTGAA	ATATGTATAT	ATCCTCCGAA	1943
678 679	መረመመው ለ ላ ላ ላ	TTAAGAATGT	7 T 7 T 7 C T C 7 7		7 CC 7 7 7 7 7 CC	CCAACACCC	2003
680	ICITIACATA	TIAAGAATGI	AIAIAGICAA	CIGGIIAAAC	AGGAAAAICI	GGAACAGCCI	2003
681	GGCTGGGTTT	TAATCTTAGC	ACCATCCTAC	TAAATGTTAA	ATAATATTAT	AATCTAATGA	2063
682							
683	ATAAATGACA	ATGCAATTCC	AAATAGAGTT	CATCTGATGA	CTTCTAGACT	CACAAAATTG	2123
684 685	CAACACACC	CA COMPONDO	TO A COURCETTO	CA A A MCA MCM			2102
686	CAAGAGAGCI	CAGTTGTTGC	TCAGTIGTIC	CAAATCATGT	CGIIIGIIAA	IIIGIAAIIA	2183
687	AGCTCCAAAG	GATGTATAGC	TACTGACAAA	AAAAAAAATG	AGAATGTAGT	TAATCCAAAT	2243
688							
689	CAAAACTTTC	CTATTGCAAT	GCGTATTTTC	TGCTTCATTA	TCCTTTAATA	TAATATTTTA	2303
690	3 COUD C C 3 3 C	m > > mmmm > > m	ma	7 7 CCCMMC7 C	3 3 mm 3 mmmm 3	7 7 M 7 M 7 7 C 7 7	2262
691 692	AGTTAGCAAG	TAATTTTAAT	TACAATGCAC	AAGCCTTGAG	AATTATTTTA	AATATAAGAA (2363
693	AATCATAATG	TTTGATAAAG	AAATCATGTA	AGAAATTTCA	AGATAATGGT	TTAACAAATA	2423
694							
695	ATTTTGTTGA	TAGAAGATAA	GACTAAAAGT	GAAATTCGAA	GTGGAGAGGA	CACTTAAACT	2483
696	CELL CELL CELL	mma mamama a	mmaaa ama aa	3 3 M 3 C M 3 3 M C	3 C C 3 C C C C C C C C C C C C C C C C	3 mmaaa3 3 am	2542
697 698	GIAGIACIIG	TTATGTGTGA	TICCAGIAAA	AATAGTAATG	AGCACTIATI	ATTGCCAAGT	2543
699	ACTGTTCTGA	GGGTACCATA	TGCAATAAGT	TATTTAATCC	TTACAATAAT	CTTGTAAGGC	2603
700							
701	AGATTCAAAC	TATCATTACA	CTTATTTTAC	AGATGAGAAA	ACTGGGGCAC	AGATAAAGCA	2663
702 703	አርጥጥርርርር እአ	GGTCTCATAG	СТСТА АСТСА	አሮሮሮሞአሮሮርሞ	CAACACCTAC	እ አርሞአርርርር አ	2723
703	ACTIGCCCAA	GGICICATAG	CIGIAAGICA	ACCCIACGGI	CAAGACCIAC	AAGTAGCCGA	2123
705	GCTCCAGAGT	ACATTATGAG	GGTCAAAGAT	TGTCTTATTA	CAAATAAATT	CCAAGTAGAA	2783
706							
707	TCAACCTTTA	ATAAGTCTTT	AATGTCTCTT	AAATATGTTT	ATATAGGAGT	CTAATCACCA	2843
708 709	አጥጥሮ አሮአ አአአ	አሞሮ እ እ እ ሮሞ እ ሮ	~~	አአሮአአሞአአሞሮ	አጥአርርአአጥርጥ	AACAATCCAA	2903
709	ATTCACAAAA	AIGAAAGIAG	GGAAAIGAII	MUMMIMAIC	AIAGGAAICI	AACAAICCAA	2703
711	GTGGCTTGAG	AATATTCATT	CTTCTTGACA	GTATAGATTC	TTTACAATTT	CGTAAGTTCC	2963
712							
713	AATGTATGTT	TTAGGAATAT	GAGGTCATTA	CTATTCATAA	TCTGATACAG	CTTTATCCTA	3023
714							

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715	AGGCCTCTCT TTAAAAACTA CACTGCATCA TAGCTTTTTT GTGCAGTTGG TCTTTCTACT	3083
716 717	GTTACTGAAC AGTAAGCAAC CTACAGATTC ACTATCACCA ACCAGCCAGT TGATGGATCT	2142
718	GITACIGAAC AGTAAGCAAC CTACAGATTC ACTATCACCA ACCAGCCAGT IGATGGATCT	3143
719 720	TAAGCAAATT ATCAAGCTTG TGATAACCTA AATTATAAAA TGAGGGTGTT GGAATAGTTA	3203
721	CATTCCAAAT CTTCTATAAC ACTCTGTATT ATATTTCTGC CTCATTCCTT GTAG GGT	3260
722	Gly	
723	·	
724		
725	TTC TTC AGT GCC CGT GGT CAT CGA CCC CTT GAC AAG AAG AGA GAA GAG	3308
726	Phe Phe Ser Ala Arg Gly His Arg Pro Leu Asp Lys Lys Arg Glu Glu	
727	40 45 50 55	
728	OCH 000 200 000 200 000 000 000 000 000 200 200 200 000 000 000 000	2256
729 730	GCT CCC AGC CTG AGG CCT GCC CCA CCG CCC ATC AGT GGA GGT GGC TAT Ala Pro Ser Leu Arg Pro Ala Pro Pro Pro Ile Ser Gly Gly Gly Tyr	3356
731	60 65 70	
732	00 65 70	
733	CGG GCT CGT CCA GCC AAA GCA GCT GCC ACT CAA AAG AAA GTA GAA AGA	3404
734	Arg Ala Arg Pro Ala Lys Ala Ala Ala Thr Gln Lys Lys Val Glu Arg	3101
735	75 80 85	
736		
737	AAA GCC CCT GAT GCT GGA GGC TGT CTT CAC GCT GAC CCA GAC CTG	3449
738	Lys Ala Pro Asp Ala Gly Gly Cys Leu His Ala Asp Pro Asp Leu	
739	90 95 100	
740		
741	GTGGGTGCAC TGATGTTTCT TGCAGTGGTG GCTCTCTCAT GCAGAGAAAG CCTGTAGTCA	3509
742		
743	TGGCAGTCTG CTAATGTTTC ACTGACCCAC ATTACCATCA CTGTTATTTT GTTTGTTTAT	3569
744		
745	TTTGGAAATA AAATTCAAAA CATAAACATA TTGGGCCTTT GGTTTAGGCT TTCTTTCTTG	3629
746		2600
747 748	TTTTCTTTGG TCTGGGCCCA AAATTTCAAA TTAGGATATG TGGGTGCCAC CTTTCCATTT	3689
749	GTATTTTGCC ACTGCCTTTG TTTAGTTGGT AAAATTTTCA TAGCCCAATT ATATTTTTTC	3749
750	GIATITIGGE ACIGCETTIG TITAGTIGGT AAAATTITCA TAGCCCAATT ATATTITITC	3/47
751	TGGGGTAAGT AATATTTTAA ATCTCTATGA GAGTATGATG ATGACTTTCG AATTTCTGGT	3809
752		0002
753	CTTACAGAAA ACCAAATAAT AAATTTTTAT GTTGGCTAAT CGTATCGCTG AATTTTCCTA	3869
754		
755	TGTGCTATTT TAACAAATGT CCATGACCCA AATCCTTCAT CTAATGCCTG CTATTTTCTT	3929
756		
757	TGTTTTTAG GGG GTG TTG TGT CCT ACA GGA TGT CAG TTG CAA GAG GCT	3977
758	Gly Val Leu Cys Pro Thr Gly Cys Gln Leu Gln Glu Ala	
759	105 110 115	
760		400-
761 762	TTG CTA CAA CAG GAA AGG CCA ATC AGA AAT AGT GTT GAT GAG TTA AAT	4025
762	Leu Leu Gln Gln Glu Arg Pro Ile Arg Asn Ser Val Asp Glu Leu Asn	
763 764	120 125 130	
765	AAC AAT GTG GAA GCT GTT TCC CAG ACC TCC TCT TCT TCC TTT CAG TAC	4073
/03	ARC ART GTG GAR GCT GTT TCC CAG ACC TCC TCT TCC TTT CAG TAC	±0/3

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766 767 768	Asn Asn Val Glu Ala Val Ser Gln Thr Ser Ser Ser Ser Phe Gln Tyr 135 140 145	
769	ATG TAT TTG CTG AAA GAC CTG TGG CAA AAG AGG CAG AAG CAA GTA AAA G	4122
770	Met Tyr Leu Leu Lys Asp Leu Trp Gln Lys Arg Gln Lys Gln Val Lys	1122
771	150 155 160	
772		
773	GTAGATATCC TTGTGCTTTC CATTCGATTT TCAGCTATAA AATTGGAACC GTTAGACTGC	4182
774		
775	CACGAGAATG CATGGTTGTG AGAAGATTAA CATTTCTGGG TTAGTGAATA GCATTCATAC	4242
776		
777	GCTTTTGGGC ACCTTCCCCT GCAACTTGCC AGATAAGCAC TATTCAGCTC TTATTCCCAG	4302
778 779	TCTGACATCA GCAAGTGTGA TTTTCTATGA AAAATTCTAC TATGACTCCT TATTTTAAGT	4362
780	TOTGACATCA GCAAGIGIGA TITTCIAIGA AAAATTCIAC TAIGACTCCI TATTTIAAGI	4302
781	ATACAAGAAA CTTGTGACTC AGAAGATAAT ATTTACAGAG TGGAAAAAAA CCCCTAGCAT	4422
782		
783	TTATAGTTTT AACATTTGAG GTTTTGAATG AGAGAGTTAT CCATAATATA TTCAATTGTG	4482
784		
785	TTGTGGATAA TGACACCTAA CCTGTGAATC TTGAGGTCAG AATGTTGAGT GCTGTTGACT	4542
786		
787	TGGTGGTCAG GAAACAGCTA GTGCGTGAGC CTGGCACAGG CATCTCAGTG AGTAGCATAC	4602
788	GG3.G3.GMTGG 3.3.2MTMTGG3 3.3.G3.3.MG3.3.3.GG3.MG3.MG 3.G3.MGMTG3.MG 3.3.2MTG3.MG	4660
789 790	CCACAGTTGG AAATTTTTCA AAGAAATCAA AGGAATCATG ACATCTTATA AATTTCAAGG	4662
791	TTCTGCTATA CTTATGTGAA ATGGATAAAT AAATCAAGCA TATCCACTCT GTAAGATTGA	4722
792	TICIOCIAIA CIIAIGIGAA AIGGAINAAI AAAICAAGCA TAICCACICI GIAAGAIIGA	4/22
793	ACTTCTCAGA TGGAAGACCC CAATACTGCT TTCTCCTCTT TTCCCTCACC AAAGAAATAA	4782
794		
795	ACAACCTATT TCATTTATTA CTGGACACAA TCTTTAGCGT ATACCTATGG TAAATTACTA	4842
796		
797	GTATGGTGGT TAGGATTTAT GTTAATTTGT ATATGTCATG CGCCAAATCA TTTCCACTAA	4902
798	101 C1	
799	ATATGACTAT ATATCATAAC TGCTTGGTGA TAGCTCAGTG TTTAATAGTT TATTCTCAGA	4962
800 801	AAATCAAAAT TGTATAGTTA AATACATTAG TTTTATGAGG CAAAAATGCT AACTATTTCT	5022
802	AAATCAAAAT TOTATAGTTA AATACATTAG TTTTATGAGG CAAAAATGCT AACTATTTCT	5022
803	ACATAATTTC ATTTTTCCAG AT AAT GAA AAT GTA GTC AAT GAG TAC TCC	5071
804	Asp Asn Glu Asn Val Val Asn Glu Tyr Ser	
805	165 170	
806		
807	TCA GAA CTG GAA AAG CAC CAA TTA TAT ATA GAT GAG ACT GTG AAT AGC	5119
808	Ser Glu Leu Glu Lys His Gln Leu Tyr Ile Asp Glu Thr Val Asn Ser	
809	175 180 185	
810		5167
811 812	AAT ATC CCA ACT AAC CTT CGT GTG CTT CGT TCA ATC CTG GAA AAC CTG Asn Ile Pro Thr Asn Leu Arg Val Leu Arg Ser Ile Leu Glu Asn Leu	270\
813	190 195 200 205	
814	200 200	
815	AGA AGC AAA ATA CAA AAG TTA GAA TCT GAT GTC TCA GCT CAA ATG GAA	5215
816	Arg Ser Lys Ile Gln Lys Leu Glu Ser Asp Val Ser Ala Gln Met Glu	

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817	210	215	220
818	210	215	220
819	TAT TGT CGC ACC CCA TGC ACT GTC AG	T TGC AAT ATT CCT GTG	GTG TCT 5263
820	Tyr Cys Arg Thr Pro Cys Thr Val Se		
821	225 239	_	
822			
823	GGC AAA G GTAACTGATT CATAAACATA T	TTTTAGAGA GTTCCAGAAG	AACTCACACA 5320
824	Gly Lys		
825	• •		
826			
827	CCAAAAATAA GAGAACAACA ACAACAACAA	AATGCTAAG TGGATTTTCC	CAACAGATCA 5380
828			
829	TAATGACATT ACAGTACATC ATAAAAATAT CO	CTTAGCCAG TTGTGTTTTG	GACTGGCCTG 5440
830			
831	GTGCATTTGC TGGTTTTGAT GAGCAGGATG G	GGCACAGGT AGTCCCAGGG	GTGGCTGATG 5500
832			
833	TGTGCATCTG CGTACTGGCT TGAACAGATG G	CAGAACCAC AGATAGATGT	AGAAGTTTCT 5560
834			
835	CCATTTTGTG TGTTCTGGGA GCTCATGGAT A	TTCCAGGAC ACAAAAGGTG	GAGAAGAGCT 5620
836			
837	TTGTTCATCC TCTTAGCAGA TAAACGTCCT C	AAAACTGGG TTGGACTTAC	TAAAGTAAAA 5680
838			
839	TGAAAATCTA ATATTTGTTA TATTATTTTC A	AAGGTCTAT AATAACACAC	TCCTTAGTAA 5740
840			
841	CTTATGTAAT GTTATTTTAA AGAATTGGTG AG	CTAAATACA AAGTAATTAT	GTCATAAACC 5800
842			
843	CCTGAACATA ATGTTGTCTT ACATTTGCAG		
844		lu Cys Glu Glu Ile Il	
845	24	40 24	5
846	GG1 GGM G11 1G1 EGT G11 1EG E11 G		
847	GGA GGT GAA ACA TCT GAA ATG TAT CTC		
848	Gly Gly Glu Thr Ser Glu Met Tyr Let	~	Ser Val
849	250 255	260	
850	777 CCC	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	G 5044
851 852	AAA CCG TAT AGA GTA TAC TGT GAC ATC		
853	Lys Pro Tyr Arg Val Tyr Cys Asp Met 265 270	-	
854	265 270	275	
855	GTAAGCTTTC GACAGTTGTT GACCTGTTGA TO	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	GTAAAATGCC 6004
856	GIAAGCIIIC GACAGIIGII GACCIGIIGA I	CIGIAATIA TIIGGATACC	GIAAAAIGCC 0004
857	AGGAAACAAG GCCAGGTGTG GTGGCTCATA C	TTGTAATTC CAGCACCTTG	GGAGGCCAAA 6064
858	AUGMACANO OCCAGOTOTO OTOGETCATA C	ordeneerid	GOAGGECAAA 0004
859	GTGGGCTGAT AGCTTGAGCC TAGGAGTTTG A	AACTAGCCT GGGCAACATA	ATGAGACCCT 6124
860			
861	AACTCTACAA AAAAAAAAAA AATACCAAAA A	AAAAAAAA AATCAGCTGT	GTTGGTAGTA 6184
862			
863	TGTGCCTGTA GTCCCAGCTA TCCAGGAGGC TO	GAGATGGGA GATCACCTGA	GCCCACAACC 6244
864			
865	TGGAGTCTTG ATCATGCTAC TGAACTGTAG C	CTGGGCAAC AGAGGATAGT	GAGATCCTGT 6304
866			
867	CTCAAAAAA AAAATTAATT AAAAAGCCAG G	AAACAAGAC TTAGCTCTAA	CATCTAACAT 6364

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868		
869	AGCTGACAAA GGAGTAATTT GATGTGGAAT TCAACCTGAT ATTTAAAAGT TATAAAATAT 6	5424
870	ACCIGACAAA GGAGIAAIII GAIGIGGAAI ICAACCIGAI AIIIAAAAGI IAIAAAAIAI 0	7424
871	CTATAATTCA CAATTTGGGG TAAGATAAAG CACTTGCAGT TTCCAAAGAT TTTACAAGTT 6	5484
872	omminist diameters in the state of the state	7101
873	TACCTCTCAT ATTTATTTCC TTATTGTGTC TATTTTAGAG CACCAAATAT ATACTAAATG 6	5544
874		,,,,,
875	GAATGGACAG GGGATTCAGA TATTATTTTC AAAGTGACAT TATTTGCTGT TGGTTAATAT 6	6604
876		
877	ATGCTCTTTT TGTTTCTGTC AACCAAAG GA TGG ACA GTG ATT CAG AAC CGT 6	655
878	Gly Trp Thr Val Ile Gln Asn Arg	
879	280 285	
880		
881	CAA GAC GGT AGT GTT GAC TTT GGC AGG AAA TGG GAT CCA TAT AAA CAG 6	5703
882	Gln Asp Gly Ser Val Asp Phe Gly Arg Lys Trp Asp Pro Tyr Lys Gln	
883	290 295 300	
884		
885	GGA TTT GGA AAT GTT GCA ACC AAC ACA GAT GGG AAG AAT TAC TGT GGC 6	3751
886	Gly Phe Gly Asn Val Ala Thr Asn Thr Asp Gly Lys Asn Tyr Cys Gly	
887	305 310 315	
888		
889	CTA CCA G GTAACGAACA GGCATGCAAA ATAAAATCAT TCTATTTGAA ATGGGATTTT 6	808
890	Leu Pro	
891		
892		
892 893	TTTTAATTAA AAAACATTCA TTGTTGGAAG CCTGTTTTAG GCAGTTAAGA GGAGTTTCCT 6	868
-	TTTTAATTAA AAAACATTCA TTGTTGGAAG CCTGTTTTAG GCAGTTAAGA GGAGTTTCCT 6	868
893		5868 5928
893 894 895 896		
893 894 895 896 897	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6	
893 894 895 896 897 898	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6	5928
893 894 895 896 897	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6	5928
893 894 895 896 897 898 899	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320	5928 5980
893 894 895 896 897 898 899 900	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7	5928
893 894 895 896 897 898 899 900 901	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7 Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu	5928 5980
893 894 895 896 897 898 899 900 901 902 903	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7	5928 5980
893 894 895 896 897 898 899 900 901 902 903 904	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 6 Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT 7	5928 5980
893 894 895 896 897 898 899 900 901 902 903 904 905 906	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT 6 Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7 Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT 7 Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT 7	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 350 355	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 350 355 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 907 908 909 910 911 912	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 365 370	5928 5980 7028 7076
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 911 912 913	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7 Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT 7 Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 350 355 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG 7 Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 365 370 AAC AAA TAC AGA GGA GCA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT 7	5928 5980 7028
893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 350 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 365 AAC AAA TAC AGA GGA ACA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met Asp Gly Ala Ser	5928 5980 7028 7076
893 894 895 896 897 898 900 901 902 903 904 905 907 909 910 911 913 914 915	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT 6 TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT 7 Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 330 335 340 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT 7 Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 350 355 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG 7 Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 365 370 AAC AAA TAC AGA GGA GCA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT 7	5928 5980 7028 7076
893 894 895 896 897 898 900 901 902 903 904 905 907 909 911 912 913 914 915 916	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 AAC AAA TAC AGA GGA ACA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met Asp Gly Ala Ser 375 380 385	5928 5980 7028 7076 7124
893 894 895 896 897 898 900 901 902 903 904 905 907 909 910 911 913 914 915	GACAAAAATG TGGAAGCTAA AGATAAGGGA AGAAAGGCAG TTTTTAGTTT CCCAAAATTT TATTTTTGGT GAGAGATTTT ATTTTGTTTT TCTTTTAG GT GAA TAT TGG CTT Gly Glu Tyr Trp Leu 320 GGA AAT GAT AAA ATT AGC CAG CTT ACC AGG ATG GGA CCC ACA GAA CTT Gly Asn Asp Lys Ile Ser Gln Leu Thr Arg Met Gly Pro Thr Glu Leu 325 TTG ATA GAA ATG GAG GAC TGG AAA GGA GAC AAA GTA AAG GCT CAC TAT Leu Ile Glu Met Glu Asp Trp Lys Gly Asp Lys Val Lys Ala His Tyr 345 GGA GGA TTC ACT GTA CAG AAT GAA GCC AAC AAA TAC CAG ATC TCA GTG Gly Gly Phe Thr Val Gln Asn Glu Ala Asn Lys Tyr Gln Ile Ser Val 360 AAC AAA TAC AGA GGA ACA GCC GGT AAT GCC CTC ATG GAT GGA GCA TCT Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met Asp Gly Ala Ser 375 380 385	5928 5980 7028 7076

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

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919 920	390	395 400	
921	TTC AGC ACG	TAT GAC AGA GAC AAT GAC GGC TG GTATGTGTGG	7262
922		Tyr Asp Arg Asp Asn Asp Gly Trp	
923	405	410 415	
924			
925	CACTCTTTGC 1	TCCTGCTTTA AAAATCACAC TAATATCATT ACTCAGAATC ATTAACAATA	A 7322
926			7202
927 928	TTTTTAATAG (CTACCACTTC CTGGGCACTT ACTGTCAGCC ACTGTCCTAA GCTCTTTAT(3 7382
929	רמיירמריירנים ז	AAGCATTTCA ACTATAAGGT AGACATTCTT ATTCTCATTT TACAGATGA	3 7442
930	CHICACICON P	ANDONITION NOTHIANDOT MORCHICIT MITCHONITI TROMONION	, 112
931	ATTTAGAGAG A	ATTACGTGAT TTGTCCAATG TCACACAACT ACCCAGAGAT AAAACTAGA	A 7502
932			
933	TTTGAGCACA C	GTTACTTTCT GAATAATGAG CATTTAGATA AATACCTATA TCTCTATAT	r 7562
934			
935	CTAAAGTGTG 1	TGTGAAAACT TTCATTTTCA TTTCCAGGGT TCTCTGATAC TAAGGGTTG	r 7622
936 937	7777CCTT7TTT 7		G 7682
937 938	AAAAGCIAII A	ATTCCAGTAT AAAGTAACAA ACACAGTCCC TAGATGGATT GCCACAAAG	3 /002
939	СССАСТТАТС Т	TCTCTTTCTT GCTATAGGGC ACAGGAGGTC TTTGGTGTAT TAGTGTGAC'	г 7742
940			- ,,,
941	CTATGTATAG C	CACCCAAAGG AAAGACTACT GTGCACACGA GTGTAGCAGT CTTTTATGG	G 7802
942			
943	TAATCTGCAA A	AACGTAACTT GACCACCGTA GTTCTGTTTC TAATAACGCC AAACACATT	r 7862
944			
945		TTA ACA TCA GAT CCC AGA AAA CAG TGT TCT AAA GAA GAC	7910
945 946		Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp	7910
945 946 947			7910
945 946 947 948	I	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 425	
945 946 947	I GGT GGT GGA	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 425 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC	7910 7958
945 946 947 948 949	I GGT GGT GGA	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 425	
945 946 947 948 949 950	GGT GGT GGA Gly Gly Gly	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 425 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly	
945 946 947 948 949 950 951	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC	
945 946 947 948 949 950 951 952 953	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 425 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 440	7958
945 946 947 948 949 950 951 952 953 954	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC	7958
945 946 947 948 949 950 951 952 953 954 955	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 450 460	7958 8006
945 946 947 948 949 950 951 952 953 954 955 956	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA	7958
945 946 947 948 949 950 951 952 953 954 955 957	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser	7958 8006
945 946 947 948 949 950 951 952 953 954 955 956 957	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA	7958 8006
945 946 947 948 949 951 952 953 954 955 956 957 958	GGT GGT GGA Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465	7958 8006 8054
945 946 947 948 949 951 952 953 954 955 956 957 960	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp	TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTG	7958 8006 8054
945 946 947 948 949 951 952 953 954 955 956 957 958	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465	7958 8006 8054
945 946 947 948 959 951 952 953 955 956 957 960 962	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 455 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTC Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln	7958 8006 8054
945 946 947 948 959 951 952 953 955 956 957 961 962 963	GGT GGT GGA Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp ATG AGG AAG Met Arg Lys	Leu Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp 420 TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 455 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTC Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln	7958 8006 8054 CCCCAA 8109
945 946 947 948 959 951 953 955 956 957 961 963 964	GGT GGT GGA Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp ATG AGG AAG Met Arg Lys	TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTC Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln 480 485	7958 8006 8054 CCCCAA 8109
945 946 947 948 950 951 953 955 955 955 955 966 965 966 967	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp ATG AGG AAG Met Arg Lys	TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTC Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln 480 485	7958 8006 8054 CCCCAA 8109
945 946 947 948 950 951 953 955 955 955 955 966 965 966	GGT GGT GGA Gly Gly Gly 430 AGA TAC TAC Arg Tyr Tyr 445 ACA GAT GAT Thr Asp Asp ATG AGG AAG Met Arg Lys TACGTAGATT T	TGG TGG TAT AAT AGA TGT CAT GCA GCC AAT CCA AAC GGC Trp Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly 435 TGG GGT GGA CAG TAC ACC TGG GAC ATG GCA AAG CAT GGC Trp Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly 450 GGT GTA GTA TGG ATG AAT TGG AAG GGG TCA TGG TAC TCA Gly Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser 465 ATG AGT ATG AAG ATC AGG CCC TTC TTC CCA CAG CAA TAGTC Met Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln 480 TTTGCTCTTC TGTATGTGAC AACATTTTTG TACATTATGT TATTGGAAT	7958 8006 8054 CCCCAA 8109 T 8169 A 8229

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

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970	TOTTO COLOR COLOR DE LA CARRA DE COLOR DE COLOR	0040
971 972	TCTTGCTCAC CCAAGAAGTA ACAAAAGTAT AGTTTTGACA GAGTTGGTGT TCATAATTTC	8349
973	AGTTCTAGTT GATTGCGAGA ATTTTCAAAT AAGGAAGAGG GGTCTTTTAT CCTTGTCGTA	8409
974	AGIICIAGII GAIIGCGAGA AIIIICAAAI AAGGAAGAGG GGICIIIIAI CCIIGICGIA	0403
975	GGAAAACCAT GACGGAAAGG AAAAACTGAT GTTTAAAAGT CCACTTTTAA AACTATATTT	8469
976	GOARARCCAI GACGGARAGG AARAACIGAI GIIIAAAAGI CCACIIIIAA AACIAIAIII	0407
977	ATTTATGTAG GATCTGTCAA AGAAAACTTC CAAAAAGATT TATTAATTAA ACCAGACTCT	8529
978	MIIIIOIAO OMICIOICAN AGRIRICITO CARRESONII INITIALITA ACCIONCICI	0323
979	GTTGCAATAA GTTAATGTTT TCTTGTTTTG TAATCCACAC ATTCAATGAG TTAGGCTTTG	8589
980		0000
981	CACTTGTAAG GAAGGAGAAG CGTTCACAAC CTCAAATAGC TAATAAACCG GTCTTGAATA	8649
982		
983	TTTGAAGATT TAAAATCTGA CTCTAGGACG GGCACGGTGG CTCACGACTA TAATCCCAAC	8709
984		
985	ACTTTGGGAG GCTGAGGCGG GCGGTCACAA GGTCAGGAGT TCAAGACCAG CCTGACCAAT	8769
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987	ATGGTGAAAC CCCATCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGCAGGTGCC	8829
988		
989	TGTAGGTCCC AGCTAGCCTG TGAGGTGGAG ATTGCATTGA GCCAAGATC	8878
990		
991		
992	(2) INFORMATION FOR SEQ ID NO:4:	
993		
994	(i) SEQUENCE CHARACTERISTICS:	
995	(A) LENGTH: 491 amino acids	
996	(B) TYPE: amino acid	
997	(D) TOPOLOGY: linear	
998	444)	
999	(ii) MOLECULE TYPE: protein	
1000	/ 1)	
1001	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
1002	Not for Jon Mat 11-1 Can Man Con Dia 11-1 Ton Ton The Mat Ton	
1003	Met Lys Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys	
1004	1 5 10 15	
1005 1006	His Leu Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly	
1005	20 25 30	
1007	20 25 50	
1008	Val Asn Asp Asn Glu Glu Gly Phe Phe Ser Ala Arg Gly His Arg Pro	
1010	-	
1011	33 30 33	
1012	Leu Asp Lys Lys Arg Glu Glu Ala Pro Ser Leu Arg Pro Ala Pro Pro	
1013	50 55 60	
1014		
1015	Pro Ile Ser Gly Gly Gly Tyr Arg Ala Arg Pro Ala Lys Ala Ala Ala	
1016	65 70 75 80	
1017		
1018	Thr Gln Lys Lys Val Glu Arg Lys Ala Pro Asp Ala Gly Gly Cys Leu	
1019	85 90 95	
1020		

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1021	His	Ala	Asp	Pro	Asp	Leu	Glv	Val	Leu	Cvs	Pro	Thr	Glv	Cvs	Gln	Leu
1022				100			1		105	-1-			1	110		
1023	_	_	_					_								
1024	Gln	Glu		Leu	Leu	Gln	Gln		Arg	Pro	Ile	Arg		Ser	Val	Asp
1025 1026			115					120					125			
1026	Glu	T.011	λan	λan	Asn	17a l	Gl 11	ת 1 ת	37-3	802	Gl n	Thr	cor	Sor	802	Cor
1027	GIU	130	ASII	ASII	ASII	vai	135	Ата	vai	Ser	GTII	140	Ser	SEI	261	Ser
1029							100									
1030	Phe	Gln	Tvr	Met	Tyr	Leu	Leu	Lvs	Asp	Leu	Trp	Gln	Lvs	Ara	Gln	Lvs
1031	145				_1 _	150					155			5		160
1032																
1033																
1034	Gln	Val	Lys	Asp	Asn	Glu	Asn	Val	Val	Asn	Glu	Tyr	Ser	Ser	Glu	Leu
1035					165					170					175	
1036	~ 1	.	•••	~ 1		m	- 1 -		~1					-	-1.	_
1037 1038	GIU	ьys	HIS		Leu	Tyr	тте	Asp		Thr	vaı	Asn	ser		тте	Pro
1038				180					185					190		
1040	Thr	Asn	Leu	Δτα	Val	Leu	Δra	Ser	Tle	T.em	Glu	Δsn	T.e.ii	Δrα	Ser	Lve
1041			195				9	200					205	••••		-75
1042																
1043	Ile	Gln	Lys	Leu	Glu	Ser	Asp	Val	Ser	Ala	Gln	Met	Glu	Tyr	Cys	Arg
1044		210					215					220				
1045																
1046		Pro	Cys	Thr	Val		Cys	Asn	Ile	Pro		Val	Ser	Gly	Lys	
1047	225					230					235					240
1048	0	a1	<i>α</i> 1	T1.	т1.	7 ~~~	T	01	a 1	a1	mb	C	a 3	Mak	TT	т
1049 1050	Cys	GIU	GIU	тте	Ile 245	Arg	ьуѕ	GIA	GTÀ	250	Inr	ser	GIU	мес	255	ьeu
1051					243					230					233	
1052	Ile	Gln	Pro	asp	Ser	Ser	Val	Lvs	Pro	Tvr	Ara	Val	Tvr	Cvs	Asp	Met
1053				260					265					270		
1054																
1055	Asn	Thr	Glu	Asn	Gly	Gly	${\tt Trp}$	Thr	Val	Ile	${\tt Gln}$	Asn	Arg	Gln	Asp	Gly
1056			275					280					285			
1057	_		_			_	_	_	_	_	_	_				
1058	Ser		Asp	Phe	GIA	Arg		Trp	Asp	Pro	Tyr	_	GIn	GTA	Phe	Gly
1059 1060		290					295					300				
1061	λen	1721	212	Thr	λen	Thr	Δen	G1 37	Tare	Δen	Туг	Cve	Glv	T.A11	Dro	Gly
1062	305	vai	AIG	1111	ASII	310	нар	GIY	цуз	ASII	315	СуБ	GLY	пец	FIO	320
1063																
1064	Glu	Tyr	Trp	Leu	Gly	Asn	Asp	Lys	Ile	Ser	Gln	Leu	Thr	Arg	Met	Gly
1065		-	-		325		_	-		330				_	335	-
1066																
1067	Pro	Thr	Glu		Leu	Ile	Glu	Met		Asp	${\tt Trp}$	Lys	Gly	_	Lys	Val
1068				340					345					350		
1069	T	7.7 -	TT	m	~ 1-	43 -	DI	m1	T7- 7	~~ ·-	3	~1	7A 71	7	T	m
1070	гÀг	ΑΙα		Tyr	GTA	GLY	Pne		val	GIn	Asn	Glu		Asn	гла	Tyr
1071			355					360					365			

RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:02:29

1072 1073	Gln Ile Ser Val Asn Lys Tyr Arg Gly Thr Ala Gly Asn Ala Leu Met	
1074	370 375 380	
1075 1076	Asp Gly Ala Ser Gln Leu Met Gly Glu Asn Arg Thr Met Thr Ile His	
1077 1078	385 390 395 400	
1078	Asn Gly Met Phe Phe Ser Thr Tyr Asp Arg Asp Asn Asp Gly Trp Leu	
1080 1081	405 410 415	
1082	Thr Ser Asp Pro Arg Lys Gln Cys Ser Lys Glu Asp Gly Gly Gly Trp	
1083 1084	420 425 430	
1085	Trp Tyr Asn Arg Cys His Ala Ala Asn Pro Asn Gly Arg Tyr Tyr Trp	
1086 1087	435 440 445	
1088	Gly Gly Gln Tyr Thr Trp Asp Met Ala Lys His Gly Thr Asp Asp Gly	
1089 1090	450 455 460	
1091	Val Val Trp Met Asn Trp Lys Gly Ser Trp Tyr Ser Met Arg Lys Met	
1092 1093	465 470 475 480	
1094	Ser Met Lys Ile Arg Pro Phe Phe Pro Gln Gln	
1095 1096	485 490	
1097		
1098 1099	(2) INFORMATION FOR SEQ ID NO:5:	
1100	(i) SEQUENCE CHARACTERISTICS:	
1101 1102	(A) LENGTH: 10564 base pairs (B) TYPE: nucleic acid	
1103	(C) STRANDEDNESS: double	
1104 1105	(D) TOPOLOGY: linear	
1106	(ii) MOLECULE TYPE: DNA (genomic)	
1107 1108		
1100	(vii) IMMEDIATE SOURCE:	
1110 1111	(B) CLONE: human fibrinogen gamma chain	
1112	(ix) FEATURE:	
1113	(A) NAME/KEY: CDS	
1114 1115	(B) LOCATION: join(17991876, 19732017, 22072390, 2510 2603, 42114341, 46454778, 57585942, 7426	
1116	7703, 93429571)	
1117 1118		
1119	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
1120 1121	CTACACACTT CTTGAAGGCA AAGGCAATGC TGAAGTCACC TTTCATGTTC AAATCATATT	60
1121	CINCACACIT CITGANGGEN ANGGENTIGE IGANGICACE IIICAIGITE MAAICAIAII	00

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1123 1124	AAAAAGTTAG	CAAGATGTAA	TTATCAGTGT	ACTATGTAAA	TCTTTGTGAA	TGATCAATAA	120
1125	TTACATATTT	TCATTATATA	TATTTTAGTA	GATAATATTT	ATATACATTC	AACATTCTAA	180
1126 1127	ATATAGAAAG	TTTACAGAGA	AAAATAAAGC	CTTTTTTCC	AATCCTGTCC	TCCACCTCTG	240
1128 1129	CATCCCATTC	TTCTTCACAG	AGGCAACTGA	TTCAAGTCAT	TACATAGTTA	TTGAGTGTTA	300
1130 1131	እርሞእር ን እርሞእ	ጥርምሞል አርሞል ር	አርረጥአጥአጥአጥ	GTTAGATGCC	CTACCCACAC	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 	360
1132	ACIACAACIA	IGITAAGTAC	AGCIAIAIAI	GITAGATGCC	GIAGCCACAG	AAAICAGIII	360
1133 1134	ACAATCTAAT	GCAGTGGATA	CAGCATGTAT	ACATATAATA	TAAGGTTGCT	ACAAATGCTA	420
1135 1136	TCTGAGGTAG	AGCTGTTTGA	AAGAATACTA	ATACTTAAAT	GTTTAATTCA	ACTGACTTGA	480
1137	TTGACAACTG	ATTAGCTGAG	TGGAAAAGAT	GGATGAGAAA	GATTGTGAGA	CTTAATTGGC	540
1138 1139	TGGTGGTATG	GTGATATGAT	TGACAATAAC	TGCTAAGTCA	GAGAGGGATA	TATTAAGGAG	600
1140 1141	GAGAAGAAA	GCAACAAATC	ጥርርጥጥጥርልጥ	GTGTTCACTT	ጥርተጥልጥልልጥጥ	ል ጥጥር ልጥጥ ልጥጥ	660
1142							
1143 1144	TACTGAATAT	GAATATTTAT	CTTTGTTTTT	GAGTCAATAA	ATATACCTTT	GTAAAGACAG	720
1145 1146	AATTAAAGTA	TTAGTATTTC	TTTCAAACTG	GAGGCATTTC	TCCCACTAAC	ATATTTCATC	780
1147	AAAACTTATA	ATAAGCTTGG	TTCCAGAGGA	AGAAATGAGG	GATAACCAAA	AATAGAGACA	840
1148 1149	TTAATAATAG	TGTAACGCCC	AGTGATAAAT	CTCAATAGGC	AGTGATGACA	GACATGTTTT	900
1150 1151	CCCAAACACA	AGGATGCTGT	AAGGGCCAAA	CAGAAATGAT	GGCCCCTCCC	CAGCACCTCA	960
1152			•				
1153 1154	TTTTGCCCCT	TCCTTCAGCT	ATGCCTCTAC	TCTCCTTTAG	ATACAAGGGA	GGTGGATTTT	1020
1155 1156	TCTCTTCTCT	GAGATAGCTT	GATGGAACCA	CAGGAACAAT	GAAGTGGGCT	CCTGGCTCTT	1080
1157 1158	TTCTCTGTGG	CAGATGGGGT	GCCATGCCCA	CCTTCAGACA	AAGGGAAGAT	TGAGCTCAAA	1140
1159	AGCTCCCTGA	GAAGTGAGAG	CCTATGAACA	TGGTTGACAC	AGAGGGACAG	GAATGTATTT	1200
1160 1161	CCAGGGTCAT	TCATTCCTGG	GAATAGTGAA	CTGGGACATG	GGGGAAGTCA	GTCTCCTCCT	1260
1162 1163	GCCACAGCCA	СРСТТОВО	ል ጥል ልጥል ልጥርም	TAACTGATCC	СТАСССТААА	ል ሞልልሞል ር ሞርሞ	1320
1164							
1165 1166	TAACTGATCC	CTAAGCTAAG	AAAGTTCTTT	TGGTAATTCA	GGTGATGGCA	GCAGGACCCA	1380
1167 1168	TCTTAAGGAT	AGACTAGGTT	TGCTTAGTTC	GAGGTCATAT	CTGTTTGCTC	TCAGCCATGT	1440
1169	ACTGGAAGAA	GTTGCATCAC	ACAGCCTCCA	GGACTGCCCT	CCTCCTCACA	GCAATGGATA	1500
1170 1171	ATGCTTCACT	AGCCTTTGCA	GATAATTTTG	GATCAGAGAA	AAAACCTTGA	GCTGGGCCAA	1560
1172 1173	AAAGGAGGAG	CTTCAACCTG	TGTGCAAAAT	CTGGGAACCT	GACAGTATAG	GTTGGGGGCC	1620
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1174 1175	AGGATGAGGA AAAAGGAACG GGAAAGACCT GCCCACCCTT CTGGTAAGGA GGCCCCGTGA	1680
1176	ADDATORODA ARABODACO COMMUNICI CICCACCCII CICCIANDOR GGCCCGIGA	1000
1177	TCAGCTCCAG CCATTTGCAG TCCTGGCTAT CCCAGGAGCT TACATAAAGG GACAATTGGA	1740
1178		
1179	GCCTGAGAGG TGACAGTGCT GACACTACAA GGCTCGGAGC TCCGGGCACT CAGACATC	1798
1180		
1181	ATG AGT TGG TCC TTG CAC CCC CGG AAT TTA ATT CTC TAC TTC TAT GCT	1846
1182 1183	Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala	
1184	1 5 10 15	
1185	CTT TTA TTT CTC TCT TCA ACA TGT GTA GCA GTAAGTGTGC TCTTCACAAA	1896
1186	Leu Leu Phe Leu Ser Ser Thr Cys Val Ala	1000
1187	20 25	
1188		
1189	ACGTTGTTTA AAATGGAAAG CTGGAAAATA AAACAGATAA TAAACTAGTG AAATTTTCGT	1956
1190		
1191	ATTTTTTCTC TTTTAG TAT GTT GCT ACC AGA GAC AAC TGC TGC ATC TTA	2005
1192	Tyr Val Ala Thr Arg Asp Asn Cys Cys Ile Leu	
1193	30 35	
1194		
1195	GAT GAA AGA TTC GTAAGTAGTT TTTATGTTTC TCCCTTTGTG TGTGAACTGG	2057
1196 1197	Asp Glu Arg Phe	
1197	40	
1199	AGAGGGGCAG AGGAATAGAA ATAATTCCCT CATAAATATC ATCTGGCACT TGTAACTTTT	
		2117
		2117
1200		
	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC	2117
1200 1201		
1200 1201 1202	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC	2177
1200 1201 1202 1203	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT	2177
1200 1201 1202 1203 1204	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys	2177
1200 1201 1202 1203 1204 1205 1206 1207	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT	2177
1200 1201 1202 1203 1204 1205 1206 1207 1208	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp	2177 2230
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT	2177 2230
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65	2177 2230 2278
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA	2177 2230
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser	2177 2230 2278
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA	2177 2230 2278
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT	2177 2230 2278
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp 90 95	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp 90 95 GAA TCA TCA AAA CCA A GTGAGAAAAAT AAAGACTACT GACCAAAAAA	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp 90 95 GAA TCA TCA AAA CCA A GTGAGAAAAAT AAAGACTACT GACCAAAAAAA Glu Ser Ser Lys Pro	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTA ATCACTGTTA TATTTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 55 60 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp 90 95 GAA TCA TCA AAA CCA A GTGAGAAAAAT AAAGACTACT GACCAAAAAA	2177 2230 2278 2326
1200 1201 1202 1203 1204 1205 1206 1207 1208 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220	TAAAAACATA GTCTAGGTTT TACCTATTTT TCTTAATAGA TTTTAAGAGT AGCATCTGTC TACATTTTTA ATCACTGTTA TATTTCAG GGT AGT TAT TGT CCA ACT ACC TGT Gly Ser Tyr Cys Pro Thr Thr Cys 45 GGC ATT GCA GAT TTC CTG TCT ACT TAT CAA ACC AAA GTA GAC AAG GAT Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys Asp 50 65 CTA CAG TCT TTG GAA GAC ATC TTA CAT CAA GTT GAA AAC AAA ACA TCA Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr Ser 70 75 80 GAA GTC AAA CAG CTG ATA AAA GCA ATC CAA CTC ACT TAT AAT CCT GAT Glu Val Lys Gln Leu Ile Lys Ala Ile Gln Leu Thr Tyr Asn Pro Asp 90 95 GAA TCA TCA AAA CCA A GTGAGAAAAAT AAAGACTACT GACCAAAAAAA Glu Ser Ser Lys Pro	2177 2230 2278 2326

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1229 1230 1231 1232	AAG TCC AGG ATA ATG TTA GAA GAA ATT ATG AAA TAT GAA GCA TCG ATT Lys Ser Arg Ile Met Leu Glu Glu Ile Met Lys Tyr Glu Ala Ser Ile 115 120 125	2580
1233 1234 1235 1236	TTA ACA CAT GAC TCA AGT ATT CG GTAAGGATTT TTGTTTTAAT TTGCTCTGCA Leu Thr His Asp Ser Ser Ile Arg 130	2633
1237 1238	AGACTGATTT AGTTTTTATT TAATATTCTA TACTTGAGTG AAAGTAATTT TTAATGTGTT	2693
1239	TTCCCCATTT ATAATATCCC AGTGACATTA TGCCTGATTA TGTTGAGCAT AGTAGAGATA	2753
1241	GAAGTTTTTA GTGCAATATA AATTATACTG GGTTATAATT GCTTATTAAT AATCACATTG	2813
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1248 1249	GCATAGTAAG GATTTTGGCT CCTAAAGTAA ATTATATTGA ATGTGGAGCA GGAAGAAACA	3053
1250 1251	TGTCTTGAGA GACTAAGTGT GGCAAATATT GCAAAGCTCA TATTGATCAT TGCAGAATGA	3113
1252 1253	ACCTGCATAG TCTCTTCCCT TCATTTGGAA GTGAATGTCT CTGTTAAAGC TTCTCAGGGA	3173
1254 1255	CTCATAAACT TTCTGAACAT AAGGTCTCAG ATACAGTTTT AATATTTTTC CCCAATTTTT	3233
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1258 1259	TGGCCCAGGA AAGATTTCTC CTCTTTTTGC TATCAGAGGG CCCTTGTTAT TATTGTTATT	3353
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1262		3473
1263 1264	TGCCTAAGAC AAGGTAGAGG GAAAACGTGG ACAAATAGTT TGTCTACCCT TTTTTACTTC	
1265 1266	AAAGAAAGAA CGGTTTATGC ATTGTAGACA GTTTTCTATC ATTTTTGGAT ATTTGCAAGC	3533
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1269 1270	TGTAACCAGA AGCATTAAAG AAGAAAGGGG AAGTATCTGT TGTTTTATTT TACATACAAT	3653
1271 1272	AACGTTCCAG ATCATGTCCC TGTGTAAGTT ATATTTTAGA TTGAAGCTTA TATGTATAGC	3713
1273 1274	CTCAGTAGAT CCACAAGTGA AAGGTATACT CCTTCAGCAC ATGTGAATTA CTGAACTGAG	3773
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1276 1277		3893
1277	GGTTGCTATC TGCTGTCCCT TATGCATAAA GTAAAAAGCA AAATGTCAAT GACATTTGCT	3893
1279	TATTGACAAG GACTTTGTTA TTTGTGTTGG GAGTTGAGAC AATATGCCCC ATTCTAAGTA	3953
1280	TATIONCANO UNCITTUTA TITUTUTUO UNCITONONE ANTATOCCCO ATTCIANGIA	3,33
1281	AAAAGATTCA GGTCCACATT GTATTCCTGT TTTAATTGAT TTTTTGATTT GTTTTTCTTT	4013
1282		
1283	TTCAAAAAGT TTATAATTTT AATTCATGTT AATTTAGTAA TATAATTTTA CATTTTCCTC	4073
1284		
1285	AAGAATGGAA TAATTTATCA GAAAGCACTT CTTAAGAAAA TACTTAGCAG TTTCCAAAGA	4133
1286		
1287	AAATATAAAA TTACTCTTCT GAAAGGAATA CTTATTTTTG TCTTCTTATT TTTGTTATCT	4193
1288	•	
1289	TATGTTTCTG TTTGTAG A TAT TTG CAG GAA ATA TAT AAT TCA AAT AAT CAA	4244
1290	Tyr Leu Gln Glu Ile Tyr Asn Ser Asn Asn Gln	
1291	135 140 145	
1292		
1293	AAG ATT GTT AAC CTG AAA GAG AAG GTA GCC CAG CTT GAA GCA CAG TGC	4292
1294	Lys Ile Val Asn Leu Lys Glu Lys Val Ala Gln Leu Glu Ala Gln Cys	
1295	150 155 160	
1296		4241
1297 1298	CAG GAA CCT TGC AAA GAC ACG GTG CAA ATC CAT GAT ATC ACT GGG AAA G	4341
1298	Gln Glu Pro Cys Lys Asp Thr Val Gln Ile His Asp Ile Thr Gly Lys	
1300	165 170 175	
1300	GTAACTGATG AAGGTTATAT TGGGATTAGG TTCATCAAAG TAAGTAATGT AAAGGAGAAA	4401
1301	GIAACIGAIG AAGGITATAI IGGGATTAGG ITCATCAAAG TAAGTAATGI AAAGGAGAAA	4401
1302	GTATGTACTG GAAAGTATAG GAATAGTTTA GAAAGTGGCT ACCCATTAAG TCTAAGAATT	4461
1304	GIAIGIACIG GAAAGIAIAG GAAIAGIIIA GAAAGIGGCI ACCCAIIAAG ICIAAGAAII	1101
1305	TCAGTTGTCT AGACCTTTCT TGAATAGCTA AAAAAAACAG TTTAAAAGGA ATGCTGATGT	4521
1306	Total	1321
1307	GAAAAGTAAG AAAATTATTC TTGGAAAATG AATAGTTTAC TACATGTTAA AAGCTATTTT	4581
1308		
1309	TCAAGGCTGG CACAGTCTTA CCTGCATTTC AAACCACAGT AAAAGTCGAT TCTCCTTCTC	4641
1310		
1311	TAG AT TGT CAA GAC ATT GCC AAT AAG GGA GCT AAA CAG AGC GGG CTT	4688
1312	Asp Cys Gln Asp Ile Ala Asn Lys Gly Ala Lys Gln Ser Gly Leu	
1313	180 185 190	
1314		
1315	TAC TTT ATT AAA CCT CTG AAA GCT AAC CAG CAA TTC TTA GTC TAC TGT	4736
1316	Tyr Phe Ile Lys Pro Leu Lys Ala Asn Gln Gln Phe Leu Val Tyr Cys	
1317	195 200 205	
1318		
1319	GAA ATC GAT GGG TCT GGA AAT GGA TGG ACT GTG TTT CAG AAG	4778
1320	Glu Ile Asp Gly Ser Gly Asn Gly Trp Thr Val Phe Gln Lys	
1321	210 215 220	
1322		
1323	GTAATTTTTT CCCCACCATG TGTATTTAAT AAATTCCTAC ATTGTTTCTG CCATATGGCA	4838
1324		
1325	GATACTTTTC TAAGCACCTT GTGAACCGTA GCTCATTTAA TCCTTGCAAT AGCCCTAAGA	4898
1326		

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1327	GGAAGGTACT TCTGTTACTC CTATTTACAG AAAAGGAAAC TGAGGCACAC AAGGTTAAAT	4958
1328		
1329	AACTTGCCCA AGACCACATA ACTAATAAGC AACAGAGTCA GCATTTGAAC CTAGGCAGTA	5018
1330		
1331	TAGTTTCAGA GTTTGTGACT TGACTCTATA TTGTACTGGC ACTGACTTTG TAGATTCATG	5078
1332		
1333	GTGGCACATA ATCATAGTAC CACAGTGACA AATAAAAAGA AGGAAACTCT TTTGTCAGGT	5138
1334	3.00m(3.3.03.0 0m(3.00mm)	F100
1335	AGGTCAAGAC CTGAGGTTTC CCATCACAAG ATGAGGAAGC CCAACACCAC CCCCCACCAC	5198
1336	CCC2 CC2 CC2	5050
1337	CCCACCACCA TCACCACCCT TTCACACACC AGAGGATACA CTTGGGCTGC TCCAAGACAA	5258
1338 1339		F220
1340	GGAACCTGTG TTGCATCTGC CACTTGCTGA TACCCACTAG GAATCTTGGC TCCTTTACTT	5318
1340	TCTGTTTACC TCCCACCACT GTTATAACTG TTTCTACAGG GGGCGCTCAG AGGGAATGAA	E270
1341	TOTGITTACC TOCCACCACT GITATAACTG TTTCTACAGG GGGCGCTCAG AGGGAATGAA	5378
1342	TGGTGGAAGC ATTAGTTGCC AGACACCGAT TGAGCAATGG GTTCCATCAT AAGTGTAAGA	5438
1344	IGGIGGAAGC AITAGIIGCC AGACACCGAI IGAGCAAIGG GIICCAICAI AAGIGIAAGA	3430
1344	ATCAGTAATA TCCAGCTAGA GTTCTGAAGT CGTCTAGGTG TCTTTTTAAT ATTACCACTC	5498
1345	AICAGIAAIA ICCAGCIAGA GIICIGAAGI CGICIAGGIG ICIIIIIAAI AIIACCACIC	3470
1347	ATTTAGAATT TATGATGTGC CAGAAACCCT CTTAAGTATT TCTCTTATAT TCTCTCTCAT	5558
1348	ATTIAGRATI TATGATGIGE CAGRACCET CTIARGIATT TETETTATAT TETETETCAT	3330
1349	GATCCTTGCA GCAACCCTAA GAAGTAACCA TCATTTTTCC TATTTGATAC ATGAGGAAAC	5618
1350	UNICCITOCA OCANCCCIAN UNAUTANCCA ICATITITICE INTITUATAC ATUNDUANAC	3010
1351	TGAGGTAGCT TGGCCAAGAT CACTTAGTTG GGAGTTGATA GAACCAGTGC TCTGTATTTT	5678
1352	TOAGGIAGET TOGECAAGAT CACTIAGITO GOAGTTOATA GAACCAGTGC TCTGTATTTT	3070
1353	TGACAAAATG TTGACAGCAT TCTCTTTACA TGCATTGATA GTCTATTTTC TCCTTTTGCT	5738
1354		3,30
1355	CTTGCAAATG TGTAATTAG AGA CTT GAT GGC AGT GTA GAT TTC AAG AAA AAC	5790
1356	Arg Leu Asp Gly Ser Val Asp Phe Lys Lys Asn	0.20
1357	225 230	
1358		
1359	TGG ATT CAA TAT AAA GAA GGA TTT GGA CAT CTG TCT CCT ACT GGC ACA	5838
1360	Trp Ile Gln Tyr Lys Glu Gly Phe Gly His Leu Ser Pro Thr Gly Thr	
1361	235 240 245	
1362		
1363	ACA GAA TTT TGG CTG GGA AAT GAG AAG ATT CAT TTG ATA AGC ACA CAG	5886
1364	Thr Glu Phe Trp Leu Gly Asn Glu Lys Ile His Leu Ile Ser Thr Gln	
1365	250 255 260 265	
1366		
1367	TCT GCC ATC CCA TAT GCA TTA AGA GTG GAA CTG GAA GAC TGG AAT GGC	5934
1368	Ser Ala Ile Pro Tyr Ala Leu Arg Val Glu Leu Glu Asp Trp Asn Gly	
1369	270 275 280	
1370		
1371	AGA ACC AG GTACTGTTTT GAAATGACTT CCAACTTTTT ATTGTAAAGA	5982
1372	Arg Thr Ser	
1373		
1374		
1375	TTGCCTGGAA TGTGCACTTT CCAACTATCA ATAGACAATG GCAAATGCAG CCTGACAAAT	6042
1376		
1377	GCAAACAGCA CATCCAGCCA CCATTTTCTC CAGGAGTCTG TTTGGTTCTT GGGCAATCCA	6102

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1270							
1378 1379	AAAAGGTAAA T	ጥርጥልጥጥር ልር	СУТСУУТСТУ	ልርጥርጥልጥጥርር	тасаатстаа	ттассстсса	6162
1380	THE HOOTPUM I	icimiicmo	Onionnicin	ACTOTATIO	inchilcing	TIACCCIGGA	0102
1381	ACCATTCAGA G	TAATAGCTA	ATTACTGAAC	TTTTAATCAG	TCCCAGGAAT	TGAGCATAAA	6222
1382							
1383	ATTATAATTT T	ATCTAGTCT	AAATTACTAT	TTCATGAAGC	AGGTATTATT	ATTAATCCCA	6282
1384							
1385 1386	TTTTATAGAT T	AACTTGCTC	AAAGTCACAT	TGCTGATAAG	TGGTAGAGGT	AGAATTCAGA	6342
1386	CTCAAGTAGT T	ጥ አለርጥጥጥአር	ласстатест	ርጥጥእ አ ር አ አ ርጥ	አጥርርጥርር ጥጥ ር	እ እ እ እ <i>ሮሮ</i> እ እ አጥ	6402
1388	CICAAGIAGI I	IAACIIIAG	AGCCIGICCI	CITAACAACI	AICCIGGIIG	AAAAGCAAAI	0402
1389	ACAGCCTCTT C	AGACTTCTC	AGTGCCTTGA	TGGCCATTTA	TTCTGTCAAA	TCATGAGCTA	6462
1390							
1391	CCCTAAAAGT A	AACCAGCTA	GCTCTTTTGA	TGATCTAGAG	${\tt GCTTCTTTTT}$	GCTTGAGATA	6522
1392							
1393	TTTGAAGGTT T	TAAGCATTG	TTACCTAATT	AAAATGCAGA	AAAATATCCA	ACCCTCTTGT	6582
1394 1395	TATGTTTAAG G	እ እ ጥ እ ሮ ጥ ሮ እ እ	እ ጥእም እ ጥጥ ረጥረ	መመርአ አ <i>አርአርአ</i>	ጥረረ እረጥጥጥጥጥ	TTTATTGCTT	6642
1396	IAIGIIIAAG G	AAIAGIGAA	AIAIAIIGIC	IICAAACACA	IGGACIIIII	TTTATTGCTT	6642
1397	GGTTGGTTTT T	AATCCAGAA	AGTGCTATAG	TCAGTAGACC	TTCTTCTAGG	AAAGGACCTT	6702
1398							
1399	CCATTTCCCA G	CCACTGGAG	ATTAGAAAAT	AAGCTAAATA	TTTTCTGGAA	ATTTCTGTTC	6762
1400							
1401	ATTCATTAAG G	CCCATCCTT	TCCCCCACTC	TATAGAAGTG	TTGTCCACTT	GCACAATTTT	6822
1402	TTTCCACCAAA C	3 3 mamamam	3 3 CMCCMMC3	CCTC2 C2TCC	mmmaa aaaa	202000220	6000
1403 1404	TTCCAGGAAA G	AAICICICI	AACICCIICA	GCTCACATGC	TTTGGACCAC	ACAGGGAAGA	6882
1405	CTTTGATTGT G'	TAATGCCCT	CAGAAGCTCT	CCTTCTTGCC	ACTACCACAC	TGATTTGAGG	6942
1406							
1407	AAGAAAATCC C'	TTTAGCACC	TAACCCTTCA	GGTGCTATGA	GTGGCTAATG	GAACTGTACC	7002
1408							
1409	TCCTTCAAGT T	TTGTGCAAT	AATTAAGGGT	CACTCACTGT	CAGATACTTT	CTGTGATCTA	7062
1410	manmanama m	amaan n an a	3 M 3 3 C 3 M M C	33003333G003	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	3 3 MM3 G3 GMG	5100
1411 1412	TGATAATGTG TO	GIGCAACAC	ATAACATTTC	AATAAAAGTA	GAAAATATGA	AATTAGAGTC	7122
1413	ATCTACACAT C'	TGGATTTGA	TCTTAGAATG	AAACAAGCAA	AAAAGCATCC	AAGTGAGTGC	7182
1414						11.010.10100	, 101
1415	AATTATTAGT T	TTCAGAGAT	GCTTCAAAGG	CTTCTAGGCC	CATCCCGGGA	AGTGTTAATG	7242
1416							
1417	AGCTGTGGAC TO	GGTTCACAT	ATCTATTGCC	TCTTGCCAGA	TTTGCAAAAA	ACTTCACTCA	7302
1418		man adamma	7 <i>0</i> 777 <i>0</i> 777	manna na nama	G	maama aa aa	7262
1419 1420	ATGAGCAAAT T	ICAGCCITA	AGAAACAAAG	TCAAAAATTC	CAAGGAAGCA	TCCTACGAAA	7362
1421	GAGGGAACTT C	TGAGATCCC	TGAGGAGGGT	CAGCATGTGA	TGGTTGTATT	TCCTTCTTCT	7422
1422							
1423	CAG T ACT GC	A GAC TAT	GCC ATG TTC	C AAG GTG GO	GA CCT GAA	GCT GAC	7468
1424		a Asp Tyr		e Lys Val Gl	_	Ala Asp	
1425	285		290		295		
1426	אאם שאם מממ	ርመክ አርካ መነ	.m. aaa maa s	, , , , , , , , , , , , , , , , , , ,	000 03m 00	T CCD CDT	7516
1427 1428	AAG TAC CGC (Lys Tyr Arg)						7516
1-120	-10 TIT ATG	Luca riir ry	- Ara Tyr I	ALA GIY	OTA VOD MIC	Y GIN WOL	

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1429 1430	300	30	05	310	
1431	GCC TTT GAT	GGC TTT GAT T	TT GGC GAT GAT CCT	AGT GAC AAG TTT TTC	7564
1432	Ala Phe Asp	Gly Phe Asp Ph	he Gly Asp Asp Pro	Ser Asp Lys Phe Phe	
1433	315	320	325	330	
1434					
1435				GAC AAT GAC AAT GAT	7612
1436	Th <u>r</u> Ser His	_	ln Phe Ser Thr Trp	Asp Asn Asp Asn Asp	
1437		335	340	345	
1438					
1439				TCT GGT TGG TGG ATG	7660
1440	Lys Phe Glu			Ser Gly Trp Trp Met	
1441 1442		350	355	360	
1442	አአሮ አአሮ ጥሮጥ	מאכ ממיד ממט מז	AT CTC AAT GGA GTT	TAT TAC CAA C	7703
1444			is Leu Asn Gly Val		//03
1445	365	nis Ala Giy ni	370	375	
1446	303		370	373	
1447	GTATGTTTTC C	CTTTCTTAGA TTCC	CAAGTTA ATGTATAGTG	TATACTATTT TCATAAAAA	7763
1448					,,,,,
1449	TAATAAATAG A	ATATGAAGAA ATGA	AAGAATA ATTTATAAAG	ATAGTAGGGA TTTTATCATG	7823
1450					
1451	TTCTTTATTT C	CAACTAAGTT CTT	TGAAACT GGAAGTGGAT	AATACCAAGT TCATGCCTAA	7883
1452					
1453	AATTAGCCCT T	ICTAAAGAAA TCC	ACCTGCT GCAAAATATC	CAGTAGTTTG GCATTATATG	7943
1454					
1455	TGAAACTATC A	ACCATCATAG CTG	GCACTGT GGGTTGTGGG	ATCTCCTTTA GACATACAAC	8003
1456					
1457	ATAAATGATC T	I'GGA'I'GGA'I'I' AACA	ATTACTA CATGGATGCT	TGTTGACACA TTAACCTGGC	8063
1458 1459	ששרכים אשרים כ	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		GTTTGGAGGA ACAGAATAAA	8123
1460	TICCCATGAG C	CITIGIGICA GAIA	ACACGCA GIGAACAGGI	GIIIGGAGGA ACAGAAIAAA	0123
1461·	GAGAAGGCAA G	ፕሮ ልሮፕሮርሞልል ሮርርር	CAGGGGT TTGTGAAAGC	TTGAGAGAAG AGACCAGTCT	8183
1462	Gridinio Germi	ocherooner coo	chodddi iididhahac	TIONOMONIO AGRECACICI	0105
1463	GAGGACAGTA G	GACACTTATT TTAC	GGATGGG GGTTGGATGA	GGAGGCTATA GTTTGCTATA	8243
1464					
1465	AGCTTGGAAT C	GGTTTGGAAC ACTO	GGTTTCA CTCACCTACC	CAGCAGTTAT GTGTGGGGAA	8303
1466					
1467	GCCTTACCGA I	TGCTAAAGGA TCC	ATGTTAC AATAATGGCA	TTATTTGGAA ATCCCAGTGG	8363
1468					
1469	TATTCCATGA A	ATAAAACCAC TATO	GAAGATA ATCCCACTCA	ACAGACTCTC CGTTGGAGAA	8423
1470					
1471	GGACAGCAAC A	ACCACCCTGG GAA	AGCCAAA CAGTCAGACC	AGACCTGTTT AGCATCAGTA	8483
1472	aarammaaam :	3 CC 3 M 3 M CM C C C C C	00ma0am 020m0aaa	A CITICUTE COA A A COA CITICOCC	0543
1473 1474	GGACTTCCCT A	ACCATATCTG CTG(GGTAGAT GAGTGAAACC	AGTGTTCCAA ACCACTCCGG	8543
1475	ርርጥጥርጥአርር አ ፣	አአሮሮአጥአርጥሮ ጥሮር፣	ምርአጥር ጥል ርርአአርአጥርአር	CAACCTTACC TCCTGATGTC	8603
1476	GCIIGIAGCA A	AACCAIAGIC ICC	DADIADAMOO AIOIROI	CARCCITACC ICCIDATGIC	5503
1477	CTAGCCAATC A	ACCAACTAGG AAAG	CTTTGCA CAGTTTATTT	AAAGTAACAG TTTGATTTTC	8663
1478	 •	,			
1479	ACAATATTTT 1	TAAATTGGAG AAA	CATAACT TATCTTTGCA	CTCACAAACC ACATAATGAG	8723

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1400		
1480 1481	AAGAAACTCT AAGGGAAAAT GCTTGATCTG TGTGACCCGG GGCGCCATGC CAGAGCTGTA	8783
1482	ANDARACICI ANDOGARARI GCIIGAICIG IGIGACCOGG GGCGCCAIGC CAGAGCIGIA	0/03
1483	GTTCATGCCA GTGTTGTGCT CTGACAAGCC TTTTACAGAA TTACATGAGA TCTGCTTCCC	8843
1484		
1485	TAGGACAAGG AGAAGGCAAA TCAACAGAGG CTGCACTTTA AAATGGAGAC ATAAAATAAC	8903
1486		
1487	ATGCCAGAAC CATTTCCTAA AGCTCCTCAA TCAACCAACA AAATTGTGCT TTCAAATAAC	8963
1488		
1489	CTGAGTTGAC CTCATCAGGA ATTTTGTGGC TCCTTCTCTT CTAACCTGCC TGAAGAAAGA	9023
1490		
1491	TGGTCCACAG CAGCTGAGTC CGGGATGGAT AAGCTTAGGG ACAGAGGCCA ATTAGGGAAC	9083
1492		01.43
1493 1494	TTTGGGTTTC TAGCCCTACT AGTAGTGAAT AAATTTAAAG TGTGGATGTG ACTATGAGTC	9143
1494	ACAGCACAGA TGTTGTTTAA TAATATGTTT ATTTTATAAA TTGATATTTT AGGAATCTTT	9203
1496	ACAGCACAGA IGIIGIIIAA IAAIAIGIII AIIIIAAAA IIGAIAIIII AGGAAICIII	9203
1497	GGAGATATTT TCAGTTAGCA GATAATACTA TAAATTTTAT GTAACTGGCA ATGCACTTCG	9263
1498	CONCRITE TONOTIACEA CATAMIACIA IMMITITAL CIMETOGEA ALGEACITEC	7203
1499	TAATAGACAG CTCTTCATAG ACTTGCAGAG GTAAAAAGAT TCCAGAATAA TGATATGTAC	9323
1500		
1501	ATCTACGACT TGTTTTAG GT GGC ACT TAC TCA AAA GCA TCT ACT CCT AAT	9373
1502	Gly Gly Thr Tyr Ser Lys Ala Ser Thr Pro Asn	
1503	380 385	
1504		
1505	GGT TAT GAT AAT GGC ATT ATT TGG GCC ACT TGG AAA ACC CGG TGG TAT	9421
1506	Gly Tyr Asp Asn Gly Ile Ile Trp Ala Thr Trp Lys Thr Arg Trp Tyr	
1507	390 395 400	
1508		
1509	TCC ATG AAG AAA ACC ACT ATG AAG ATA ATC CCA TTC AAC AGA CTC ACA	9469
1510	Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro Phe Asn Arg Leu Thr	
1511	405 410 415	
1512	AMM GGA GAA GGA GAG GAA GAG GAG GAG GGA GGG AAA GAG GMG AGA	0517
1513 1514	ATT GGA GAA GGA CAG CAA CAC CTG GGG GGA GCC AAA CAG GTC AGA	9517
1514	Ile Gly Glu Gly Gln His His Leu Gly Gly Ala Lys Gln Val Arg 420 425 430 435	
1516	420 423 430 433	
1517	CCA GAG CAC CCT GCG GAA ACA GAA TAT GAC TCA CTT TAC CCT GAG GAT	9565
1518	Pro Glu His Pro Ala Glu Thr Glu Tyr Asp Ser Leu Tyr Pro Glu Asp	7505
1519	440 445 450	
1520		
1521	GAT TTG TAGAAAATTA ACTGCTAACT TCTATTGACC CACAAAGTTT CAGAAATTCT	9621
1522	Asp Leu	
1523	- -	
1524	•	
1525	CTGAAAGTTT CTTCCTTTTT TCTCTTACTA TATTTATTGA TTTCAAGTCT TCTATTAAGG	9681
1526		
1527	ACATTTAGCC TTCAATGGAA ATTAAAACTC ATTTAGGACT GTATTTCCAA ATTACTGATA	9741
1528		
1529	TCAGAGTTAT TTAAAAATTG TTTATTTGAG GAGATAACAT TTCAACTTTG TTCCTAAATA	9801
1530		

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1531	TATAATAATA AAATGATTGA CTTTATTTGC ATTTTTATGA CCACTTGTCA TTTATTTTGT	9861
1532 1533	CTTCGTAAAT TATTTTCATT ATATCAAATA TTTTAGTATG TACTTAATAA AATAGGAGAA	9921
1534		
1535 1536	CATTTTAGAG TTTCAAATTC CCAGGTATTT TCCTTGTTTA TTACCCCTAA ATCATTCCTA	9981
1537	TTTAATTCTT CTTTTTAAAT GGAGAAAATT ATGTCTTTTT AATATGGTTT TTGTTTTGTT	10041
1538		
1539 1540	ATATATTCAC AGGCTGGAGA CGTTTAAAAG ACCGTTTCAA AAGAGATTTA CTTTTTTAAA	10101
1541	GGACTTTATC TGAACAGAGA GATATAATAT TTTTCCTATT GGACAATGGA CTTGCAAAGC	10161
1542 1543		10001
1543	TTCACTTCAT TTTAAGAGCA AAAGACCCCA TGTTGAAAAC TCCATAACAG TTTTATGCTG	10221
1545	ATGATAATTT ATCTACATGC ATTTCAATAA ACCTTTTGTT TCCTAAGACT AGATACATGG	10281
1546 1547	TACCTTTATT GACCATTAAA AAACCACCAC TTTTTGCCAA TTTACCAATT ACAATTGGGC	10341
1548	TACCITTATI GACCATTAAA AAACCACCAC TITTIGCCAA TITACCAATT ACAATTGGGC	10341
1549	AACCATCAGT AGTAATTGAG TCCTCATTTT ATGCTAAATG TTATGCCTAA CTCTTTGGGA	10401
1550 1551	GTTACAAAGG AAATAGCAAT TATGGCTTTT GCCCTCTAGG AGATACAGGA CAAATACAGG	10461
1552	ormania in income in incom	10101
1553	AAAATACAGC AACCCAAACT GACAATACTC TATACAAGAA CATAATCACT AAGCAGGAGT	10521
1554 1555	CACAGCCACA CAACCAAGAT GCATAGTATC CAAAGTGCAG CTG	10564
1556		
1557 1558	(2) INFORMATION FOR SEQ ID NO:6:	
1559	(2) INFORMATION FOR SEQ ID NO:6:	
1560	(i) SEQUENCE CHARACTERISTICS:	
1561	(A) LENGTH: 453 amino acids	
1562	(B) TYPE: amino acid	
1563 1564	(D) TOPOLOGY: linear	
1565	(ii) MOLECULE TYPE: protein	
1566	(II) Moddeodd IIId. piotein	
1567	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
1568		
1569	Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala	
1570	1 5 10 15	
1571		
1572	Leu Leu Phe Leu Ser Ser Thr Cys Val Ala Tyr Val Ala Thr Arg Asp	
1573 1574	20 25 30	
1575	Asn Cys Cys Ile Leu Asp Glu Arg Phe Gly Ser Tyr Cys Pro Thr Thr	
1576	35 40 45	
1577	10 40	
1578	Cys Gly Ile Ala Asp Phe Leu Ser Thr Tyr Gln Thr Lys Val Asp Lys	
1579	50 55 60	
1580 1581	Asp Leu Gln Ser Leu Glu Asp Ile Leu His Gln Val Glu Asn Lys Thr	

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1582	65					70					75					80
1583																
1584	Ser	Glu	Val	Lys	Gln	Leu	Ile	Lys	Ala	Ile	Gln	Leu	Thr	Tyr	Asn	Pro
1585					85					90					95	
1586																
1587	Asp	Glu	Ser	Ser	Lys	Pro	Asn	Met	Ile	Asp	Ala	Ala	Thr	Leu	Lys	Ser
1588				100					105					110	_	
1589																
1590	Arg	Ile	Met	Leu	Glu	Glu	Ile	Met	Lys	Tyr	Glu	Ala	Ser	Ile	Leu	Thr
1591			115					120	_	_			125			
1592																
1593	His	Asp	Ser	Ser	Ile	Arg	Tyr	Leu	Gln	Glu	Ile	Tyr	Asn	Ser	Asn	Asn
1594		130					135					140				
1595																
1596	Gln	Lys	Ile	Val	Asn	Leu	Lys	Glu	Lys	Val	Ala	Gln	Leu	Glu	Ala	Gln
1597	145					150					155					160
1598																
1599	Cys	Gln	Glu	Pro	Cys	Lys	Asp	Thr	Val	Gln	Ile	His	Asp	Ile	Thr	Gly
1600					165					170					175	
1601																
1602	Lys	Asp	Cys	Gln	Asp	Ile	Ala	Asn	Lys	Gly	Ala	Lys	Gln	Ser	Gly	Leu
1603				180					185					190		
1604																
1605	Tyr	Phe	Ile	Lys	Pro	Leu	Lys	Ala	Asn	Gln	Gln	Phe	Leu	Val	Tyr	Cys
1606			195					200					205			
1607																
1608	Glu	Ile	Asp	Gly	Ser	Gly	Asn	Gly	Trp	Thr	Val	Phe	Gln	Lys	Arg	Leu
1609		210					215					220				
1610																
1611		Gly	Ser	Val	Asp	Phe	Lys	Lys	Asn	\mathtt{Trp}	Ile	Gln	Tyr	Lys	Glu	Gly
1612	225					230					235					240
1613		_						_								
1614	Phe	Gly	His	Leu	Ser	Pro	Thr	Gly	Thr		Glu	Phe	Trp	Leu	_	Asn
1615					245					250					255	
1616		_		•	_						_	_			_	
1617	Glu	Lys	Ile		Leu	Ile	Ser	Thr		Ser	Ala	Ile	Pro	_	Ala	Leu
1618				260					265					270		
1619	_		~-	_		_	_	_		_		_			_	
1620	Arg	Val		Leu	Glu	Asp	Trp		GLŸ	Arg	Thr	Ser		Ala	Asp	Tyr
1621			275					280					285			
1622			-1		1		_			_	_	_	_	_		_
1623	Ата		Pne	ьуs	Val	GIY		GIu	Ата	Asp	ьys		Arg	Leu	Inr	Tyr
1624		290					295					300				
1625	7 .7 -	ш	Dl	77 -	~ 1=-	~ 1-	70	7.7 -	~ 1	7	77 -	Dl	7	~1 - ·	nl	7
1626		ıyr	rne	Αια	Gly	_	Asp	АТА	GTĀ	Asp		rne	Asp	GΤĀ	rne	_
1627 1628	305					310					315					320
	Dho	G1	7 ~~	7\~~	Droc	C.~	7 ~~	T	Dha	Dha	Th∽	C.~	u: ~	7 ~~	G1	Me+
1629 1630	FILE	GTÀ	Asp	Asp	Pro	ser	Asp	гуя	rne		THE	ser	пты	HSII	-	MEC
1631					325					330					335	
1632	Gl n	Dhe	Ser	Thr	Trp	Λαν	702	λαν	7 cr	7 02	Larg	Dha	<u> </u>	G1.,	Λαν	Cvc
1032	CTII	F 116	OGI	T 11T	ıτb	тэБ	LOII	Tob	voii	rob	пys	E 11G	GIU	GIA	TOIL	Cys

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1633			340					345					350			
1634 1635	710 Cl.	71 -	7	01	C	~1	(T)	(T)	M	7	T		77.º ~	77-	~ 1	
1636	Ala Glu	355	Asp	GLY	ser	GIY	360	пр	Mec	ASII	ьуѕ	365	HIS	Ата	GIA	
1637		333					300					303				
1638	His Leu	Δen	Glv	Val	Туг	Туг	Gln	Glv	Glv	Thr	ጥነሪዮ	Ser	Larg	Δla	Sar	
1639	370	HOII	Gry	Vai	TYL	375	GIII	Gry	GLY	1111	380	Ser	цуз	Ата	Ser	
1640	3,0					9,3					500					
1641	Thr Pro	Asn	Glv	Tvr	Asp	Asn	Glv	Tle	Tle	Trp	Ala	Thr	Tro	Lvs	Thr	
1642	385		0-1	-1-	390		<u></u> ,			395				-,-	400	
1643										0,0					100	
1644	Arg Trp	Tvr	Ser	Met	Lvs	Lvs	Thr	Thr	Met	Lvs	Ile	Ile	Pro	Phe	Asn	
1645	5 F	-1-		405	-1-	-1-			410	-1-				415		
1646																
1647	Arg Leu	Thr	Ile	Glv	Glu	Glv	Gln	Gln	His	His	Leu	Glv	Glv	Ala	Lvs	
1648	J		420	1		1		425				1	430		-1-	
1649																
1650	Gln Val	Arq	Pro	Glu	His	Pro	Ala	Glu	Thr	Glu	Tvr	Asp	Ser	Leu	Tvr	
1651		435					440				1	445			-1 -	
1652																
1653	Pro Glu	Asp	Asp	Leu												
1654	450	_	-													
1655																
1656	(2) INF	ORMA'	rion	FOR	SEQ	ID I	NO:7	:								
1657																
1658	(i) SE	QUEN	CE CE	IARA	CTER:	ISTI	CS:								
1659		(2	A) L	ENGTI	H: 10	0807	base	pa:	irs							
1660		(1	B) T	YPE:	nuc.	leic	acio	i								
1661		((C) S'	TRANI	DEDNI	ESS:	doub	ole								
1662		(1	D) T(OPOLO	GY:	line	ear									
1663																
1664																
1665	(vii			ATE S												
1666		(1	B) C	LONE :	ov:	ine l	oeta-	-lact	toglo	bul:	in					
1667																
1668																
1669	(xi) SE(QUEN	CE DE	ESCR:	IPTI	ON: S	SEQ :	ID N	0:7:						
1670																
1671	ACGCGTG'	TCG A	ACCT(GCAG	FT C	AACG(GATC:	r CT	GTGT(CTGT	TTTC	CATG	TA (GTAC(CACACT	60
1672																
1673	GTTTTGG	TGG (CTGT	AGCT	I'T C	AGCTZ	ACAG'	r cr	GAAG'	rcat	AAA(3CCT(GT A	ACCT(CCAGCT	120
1674	~~~~~			~									~~~	~~ ~~ :		
1675	CTGTTCT	CTC '	I'CAA(GATTC	FT G	rtct(3CTG	r TT	3GGT(CTTT	AGT	FTCT(CCA (CACA	ATTTT	180
1676	3.033mm~		~mm~-	TI N C C C C		7m~ -		n ~		705		n		~ » m····		
1677	AGAATTG	TTT (TTC!	rag'i".	rc T	JTGA	AAAA'.	ı GA'	rGCT(JG'I'A	T"I"I".	ı GATA	AAG ('I'TA¿	JCATTG	240
1678	7 7 m/m/m/m	7.71.72 -	~~m~	~~~~	D 20 CT-	a ama	n mm~	, am		73 CM	03 C	י א נחוחה		א ווו א וווי	T N N C T C	
1679	AATCTGT.	AAA (JCTA(CAGA'.	IA TA	AGTC	4.1.1.G(בים ב	AGTA(LAG I	CAC	LTTA	ACA A	ATAT"	TAACTC	300
1680	mma a ca m	ama r	TC 7 C	~ n m~ 1	\m >r	חא שנהי	nmaa.	- aa	nam» r	חאותים	א תווייטיו	י איט חווים	, mm -	aama	~m~m~~	260
1681	TTCACAT	CIG :	I GAG	CATGA	AI A	LATT.	TTCCC	J CC.	ICTA.	IAIC	ATC.	LICA	AT.T.	CCTC	CTATCA	360
1682 1683	Chhunchin	י גיטיחי	ייייטרים.	المست	מים כיו	חר א כיו	י אריי איז	7 Cm	ግጠጠ <i>ን</i> /	מאממ	THOO	השכוכים	י מיחים	~ » (-m-	~ 7 mm~~	420
TOOR	GTTTCTT	LCA :	1160	MG I I.	LI C	I GAG	I ACA(a GT	LITA	LACC	TCC.	1166	TIA (JAGT(CATTCC	420

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1684							
1685 1686	TCAGTATTTT	ATTCCTTTGA	TACAATTGTG	AATGAGGTAA	TTTTCTTAGT	TTCTCTTTCT	480
1687 1688	GATAGCTCAT	TGTTAGTGTA	TATATAGAAA	AGCAACAGAT	TTCTATGTAT	TAATTTTGTA	540
1689 1690	TCCTGCAACA	GATTTCTATG	TATTAATTTT	GTATCCTGCT	ACTTTACGGA	ATTCACTTAT	600
1691 1692	TAGCTTTTTG	GTGACATCTT	GAGGATTTTC	TGAAGAAAAT	GGCATGGTAT	GGTAGGACAA	660
1693 1694	GGTGTCATGT	CATCTGCAAA	CAGTGGCAĢT	TTTCCTTCTT	CCCTTCCAAC	CTGGATTTCT	720
1695 1696		TCTGTCTGAG					780
1697 1698		ATCCTTGTCT					840
1699 1700		AATGTTTACT					900
1701 1702 1703		TGCATCTATT				ATTTTGTCAA	960 1020
1704 1705		TTAATGATTT					1020
1706 1707		ACCTTTGTAT					1140
1708 1709		CACTTTGCTA					1200
1710 1711	TATTGGCCTA	AGAAAGGTTT	TGTCTGGTTT	TAGTATCAGG	GTGATGCTGG	CCTCATAGAG	1260
1712 1713	AGAGTTTAGA	AGCATTTCCT	CCTCTTTGAT	TTTTCGGAAT	AGTTTGAGTA	GGATAGGTAT	1320
1714 1715	TAACTCTTCT	TTAAATGTTT	GGGGACTTCC	CTGGTGAGCC	GGTGGTTGAG	AATCCGCCTC	1380
1716 1717 1718	AGGGATGTGG	GTTTGATCCC	TGGTCAGGGA	ACCATTAATA	AGATCCCACA	TGCTGCAGGC	1440
1719 1720	AACAAGCCCC	CAAGCTGCAA	CCACTGAGCT	GCAACCGCTG	CAGTGCCCAC	AGGCCACGAC	1500
1721 1722	CAGAGAAAGC	CCACATACAG	CAGGGAAGAC	CCAGCACAAC	CGGAAAAAGG	AGTTTGGTGG	1560
1723 1724	AATACAGCTG	TGAAGCCGTC	TGGTCCTGGA	CTCCTGCTTG	AGGGAATTTT	TTAAAAATTA	1620
1725 1726	TTGATTCAAT	TTCATTACTG	GTAACTGGTC	TGTTCATATT	TTCTATTTCT	TCCGGGTTCA	1680
1727 1728		ATTGTACATG					1740
1729 1730		TGGGAGCACA					1800
1731 1732		CCCAAGCAGC					1860
1733 1734	AGCCCCACAA	TTTCATTCTG	AGAAGTGATT	CCTTGCTTCT	GCACTTACAG	GCCCAGGATC	1920

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1735	TGACCTGCTT	CTGAGGAGCA	GGGGTTTTGG	CAGGACGGGG	AGATGCTGAG	AGCCGACGGG	1980
1736 1737	GGTCCAGGTC	CCCTCCCAGG	СССССТСТС	TGGGGCAGCC	СТТСССАААС	ATTGCCCCAG	2040
1738	0010010010	cccrccinco	0000001010	10000011000	CIICCOIRE	ATTOCCCCAG	2040
1739 1740	TCTCCCTCCT	ACAGTGGTCA	GTCCCAGCTG	CCCCAGGCCA	GAGCTGCTTT	ATTTCCGTCT	2100
1741	CTCTCTCTGG	ATGGTATTCT	CTGGAAGCTG	AAGGTTCCTG	AAGTTATGAA	TAGCTTTGCC	2160
1742 1743	CTGAAGGGCA	TGGTTTGTGG	TCACGGTTCA	CAGGAACTTG	GGAGACCCTG	CAGCTCAGAC	2220
1744							
1745	GTCCCGAGAT	TGGTGGCACC	CAGATTTCCT	AAGCTCGCTG	GGGAACAGGG	CGCTTGTTTC	2280
1746							
1747	TCCCTGGCTG	ACCTCCCTCC	TCCCTGCATC	ACCCAGTTCT	GAAAGCAGAG	CGGTGCTGGG	2340
1748 1749	CTCACACCCT	CTCGCATCTA	N CCCCCCTCTT	CCAAACCACC	CCTCCTCCTC	TTTCCCCCCCC	2400
1750	GICACAGCCI	CICGCAICIA	ACGCCGGIGI	CCAAACCACC	CGIGCIGGIG	110000000	2400
1751	TACCTATGGG	GAAGGGCTTC	TCACTGCAGT	GGTGCCCCC	GTCCCCTCTG	AGATCAGAAG	2460
1752		GILIGOGOTIC	renerounor	001000000	0100001010	710711 07107210	2400
1753	TCCCAGTCCG	GACGTCAAAC	AGGCCGAGCT	CCCTCCAGAG	GCTCCAGGGA	GGGATCCTTG	2520
1754							
1755	CCCCCCGCT	GCTGCCTCCA	GCTCCTGGTG	CCGCACCCTT	GAGCCTGATC	TTGTAGACGC	2580
1756							
1757	CTCAGTCTAG	TCTCTGCCTC	CGTGTTCACA	CGCCTTCTCC	CCATGTCCCC	TCCGTGTCCC	2640
1758							
1759	CGTTTTCTCT	CACAAGGACA	CCGGACATTA	GATTAGCCCC	TGTTCCAGCC	TCACCTGAAC	2700
1760							
1761	AGCTCACATC	TGTAAAGACC	TAGATTCCAA	ACAAGATTCC	AACCTGAAGT	TCCCGGTGGA	2760
1762		~~~~~~					
1763	TGTGAGTTCT	GGGGCGACAT	CCTTCAACCC	CATCACAGCT	TGCAGTTCAT	CGCAAAACAT	2820
1764 1765	CCAACCTCCC	COOTON	3 3 3 CCC3 CCT	mamman man n	3 C3 CEC 3 CCE	maaa aaamma	2000
1766	GGAACCIGGG	GTTTATCGTA	AAACCCAGGI	ICIICAIGAA	ACACIGAGCI	TCGAGGCTTG	2880
1767	ттссаасаат	TAAAGGTGCT	ΔΔΤΔCΔGΔΤC	AGGGCAAGGA	СТСААССТСС	СТАВСССТСС	2940
1768	1100111111		11111101101110	MOCCHACCH	CIGHACCIGO	CIPACCICC	2510
1769	TCTTTCCATC	ACAGGAAAGG	GGGGCCTGGG	GGCGGCTGGA	GGTCTGCTCC	CGTGAGTGAG	3000
1770							
1771	CTCTTTCCTG	CTACAGTCAC	CAACAGTCTC	TCTGGGAAGG	AAACCAGAGG	CCAGAGAGCA	3060
1772							
1773	AGCCGGAGCT	AGTTTAGGAG	ACCCCTGAAC	CTCCACCCAA	GATGCTGACC	AGCCAGCGGG	3120
1774							
1775	CCCCCTGGAA	AGACCCTACA	GTTCAGGGGG	GAAGAGGGC	TGACCCGCCA	GGTCCCTGCT	3180
1776							
1777	ATCAGGAGAC	ATCCCCGCTA	TCAGGAGATT	CCCCCACCTT	GCTCCCGTTC	CCCTATCCCA	3240
1778	A MIN COCCOON C	aaar aaaama	man man aan a	mmma	ma	7 CEC 7 7 CCCE	2200
1779 1780	ATACGCCCAC	CCCACCCCTG	TGATGAGCAG	TTTAGTCACT	TAGAATGTCA	ACTGAAGGCT	3300
1780	ጥጥርር አጥርር ር	CTTTGCCAGA	GGCACAAGGC	ACCCACAGCC	тастасатас	ССУСССССУТ	3360
1782	IIIGGAIGG	CITICCAGA	JOCACAAGGC	ccacaccc	TOCTOGGIAC	COACOCCAI	5500
1783	GTGGATTCAG	CCAGGAGGCC	TGTCCTGCAC	CCTCCCTGCT	CGGGCCCCCT	CTGTGCTCAG	3420
1784							
1785	CAACACACCC	AGCACCAGCA	TTCCCGCTGC	TCCTGAGGTC	TGCAGGCAGC	TCGCTGTAGC	3480

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1786							
1787 1788	CTGAGCGGTG	TGGAGGGAAG	TGTCCTGGGA	GATTTAAAAT	GTGAGAGGCG	GGAGGTGGGA	3540
1789 1790	GGTTGGGCCC	TGTGGGCCTG	CCCATCCCAC	GTGCCTGCAT	TAGCCCCAGT	GCTGCTCAGC	3600
1791 1792	CGTGCCCCCG	CCGCAGGGGT	CAGGTCACTT	TCCCGTCCTG	GGGTTATTAT	GACTCTTGTC	3660
1793 1794	ATTGCCATTG	CCATTTTTGC	TACCCTAACT	GGGCAGCAGG	TGCTTGCAGA	GCCCTCGATA	3720
1795 1796	CCGACCAGGT	CCTCCCTCGG	AGCTCGACCT	GAACCCCATG	TCACCCTTGC	CCCAGCCTGC	3780
1797 1798	AGAGGGTGGG	TGACTGCAGA	GATCCCTTCA	CCCAAGGCCA	CGGTCACATG	GTTTGGAGGA	3840
1799 1800	GCTGGTGCCC	AAGGCAGAGG	CCACCCTCCA	GGACACACCT	GTCCCCAGTG	CTGGCTCTGA	3900
1801 1802	CCTGTCCTTG	TCTAAGAGGC	TGACCCCGGA	AGTGTTCCTG	GCACTGGCAG	CCAGCCTGGA	3960
1803 1804	CCCAGAGTCC	AGACACCCAC	CTGTGCCCCC	GCTTCTGGGG	TCTACCAGGA	ACCGTCTAGG	4020
1805 1806	CCCAGAGGGG	ACTTCCTGCT	TGGCCTTGGA	TGGAAGAAGG	CCTCCTATTG	TCCTCGTAGA	4080
1807 1808	GGAAGCCACC	CCGGGGCCTG	AGGATGAGCC	AAGTGGGATT	CCGGGAACCG	CGTGGCTGGG	4140
1809 1810	GGCCCAGCCC	GGGCTGGCTG	GCCTGCATGC	CTCCTGTATA	AGGCCCCAAG	CCTGCTGTCT	4200
1811 1812	CAGCCCTCCA	CTCCCTGCAG	AGCTCAGAAG	CACGACCCCA	GGGATATCCC	TGCAGCCATG	4260
1813 1814	AAGTGCCTCC	TGCTTGCCCT	GGGCCTGGCC	CTCGCCTGTG	GCGTCCAGGC	CATCATCGTC	4320
1815 1816	ACCCAGACCA	TGAAAGGCCT	GGACATCCAG	AAGGTTCGAG	GGTTGGCCGG	GTGGGTGAGT	4380
1817 1818	TGCAGGGCGG	GCAGGGGAGC	TGGGCCTCAG	AGAGCCAAGA	GAGGCTGTGA	CGTTGGGTTC	4440
1819 1820	CCATCAGTCA	GCTAGGGCCA	CCTGACAAAT	CCCCGCTGGG	GCAGCTTCAA	CCAGGCGTTC	4500
1821 1822	ACTGTCTTGC	ATTCTGGAGG	CTGGAAGCCC	AAGATCCAGG	TGTTGGCAGG	GCTGGCTTCT	4560
1823 1824	CCTGCGGCCG	CTCTCTGGGG	AGCAGACGGC	CGTCTTCTCC	AGTCCTCTGC	ĞCGCCCTGAT	4620
1825 1826	TTCCTCTTCC	TGTGAGGCCA	CCAGGCCTGC	TGGAAACACG	CCTGCCTGCG	CAGCTTCACA	4680
1827 1828	CGACCTTTGT	CATCTCTTTA	AAGGCCATGT	CTCCAGAGTC	ATGTGTTGAA	GTTCTGGGGG	4740
1829 1830	TTAGTGGGAC	ACAGTTCAGC	CCCTAAAAGA	GTCTCTCTGC	CCCTCAAATT	TTCCCCACCT	4800
1831 1832	CCAGCCATGT	CTCCCCAAGA	TCCAAATGTT	GCTACATGTG	GGGGGGCTCA	TCTGGGTCCC	4860
1833 1834	TCTTTGGGTT	CAGTGTGAGT	CTGGGGAGAG	CATTCCCCAG	GGTGCAGAGT	TGGGGGGAGT	4920
1835 1836	ATCTCAGGGC	TGCCCAGGCC	GGGGTGGGAC	AGAGAGCCCA	CTGTGGGGCT	GGGGGCCCCT	4980

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1837	TCCCACCCC	AGAGTGCAAC	TCAAGGTCCC	TCTCCAGGTG	GCGGGGACTT	GGCACTCCTT	5040
1838 1839	GGCTATGGCG	GCCAGCGACA	TCTCCCTGCT	GGATGCCCAG	AGTGCCCCCC	TGAGAGTGTA	5100
1840 1841	ССТССАССАС	CTGAAGCCCA	CCCCCGAGGG	СУУССТССУС	ътестастас	AGAAATGGTG	5160
1842	CGIGGAGGAG	CIGAAGCCCA	CCCCCGAGGG	CAACCIGGAG	AICCIGCIGC	AGAAAIGGIG	3100
1843 1844	GGCGTCTCTC	CCCAACATGG	AACCCCCACT	CCCCAGGGCT	GTGGACCCCC	CGGGGGGTGG	5220
1845	GGTGCAGGAG	GGACCAGGGC	CCCAGGGCTG	GGGAAGAGGG	CTCAGAGTTT	ACTGGTACCC	5280
1846	GGGGGGGGG	aaaaamaa					
1847 1848	GGCGCTCCAC	CCAAGGCTGC	CCACCCAGGG	CTTTTTTTT	TTTTAAACTT	TTATTAATTT	5340
1849	GATGCTTCAG	AACATCATCA	AACAAATGAA	CATAAAACAT	TCATTTTTGT	TTACTTGGAA	5400
1850 1851	CCCCACATAA	AATCCTCTGA	አርፕርርእ አለፕር	СУДУССУУУС	አ ሞአሮአሞአሮአአ	талааслаат	5460
1852	GGGGAGATAA	AAICCICIGA	AGIGGAAAIG	CATAGCAAAG	ATACATACAA	1GAGGCAGG1	3400
1853	ATTCTGAATT	CCCTGTTAGT	CTGAGGATTA	CAAGTGTATT	TGAGCAACAG	AGAGACATTT	5520
1854 1855	TCATCATTTC	TAGTCTGAAC	ACCTCAGTAT	CTAAAATGAA	CAAGAAGTCC	TGGAAACGAA	5580
1856							
1857 1858	GCAGTGTGGG	GATAGGCCCG	TGTGAAGGCT	GCTGGGAGGC	AGCAGACCTG	GGTCTTCGGG	5640
1859	CTCAAGCAGT	TCCCGCTACC	AGCCCTGTCC	ACCTCAGACG	GGGGTCAGGG	TGCAGGAGAG	5700
1860							
1861 1862	AGCTGGATGG	GTGTGGGGGC	AGAGATGGGG	ACCTGAACCC	CAGGGCTGCC	TTTTGGGGGT	5760
1863	GCCTGTGGTC	AAGGCTCTCC	CTGACCTTTT	CTCTCTGGCT	TCATCTGACT	TCTCCTGGCC	5820
1864 1865	CATCCACCCG	GTCCCCTGTG	СССТСАССТС	ACAGTGAGTG	CCCCCACCCT	AGTTGGCCAG	5880
1866	CATCCACCCG	dicccidid	decidaddid	ACAGIGAGIG	CGCCGAGGCI	AGTIGGCCAG	3000
1867 1868	CTGGCTCCTA	TGCCCATGCC	ACCCCCCTCC	AGCCCTCCTG	GGCCAGCTTC	TGCCCCTGGC	5940
1869	CCTCAGTTCA	TCCTGATGAA	AATGGTCCAT	GCCAATGGCT	CAGAAAGCAG	CTGTCTTTCA	6000
1870							
1871 1872	GGGAGAACGG	CGAGTGTGCT	CAGAAGAAGA	TTATTGCAGA	AAAAACCAAG	ATCCCTGCGG	6060
1873	TGTTCAAGAT	CGATGGTGAG	TCCGGGTCCC	TGGGGGACAC	CCACCACCCC	CGCCCCGGG	6120
1874 1875	САСТСТССАС	AGGTTCAGGG	СССТССССТС	СССССТССС	אייככידא אכככ כ	АСТССТССТС	6180
1876	GACTGTGGAC	AGGTTCAGGG	GGCIGGCGIC	GGGCCCIGGG	AIGCIAAGGG	ACIGGIGGIG	0180
1877	ATGAAGACAC	TGCCTTGACA	CCTGCTTCAC	TTGCCTCCCC	TGCCACCTGC	CCGGGGCCTT	6240
1878 1879	GGGGCGGTGG	CCATGGGCAG	GTCCCGGCTG	GCGGGCTAAC	CCACCAGGGT	GACACCCGAG	6300
1880							
1881 1882	CTCTCTTTGC	TGGGGGGCGG	GCGGTGCTCT	GGGCCCTCAG	GCTGAGCTCA	GGAGGTACCT	6360
1883	GTGCCCTCCC	AGGGGTAACC	GAGAGCCGTT	GCCCACTCCA	GGGGCCCAGG	TGCCCCACGA	6420
1884 1885	CCCCAGCCCG	СТССАСАССТ	CCTTCNTCTC	СТССАСАСА	እርጥርጥ <u>ር</u> ጥርርር	CCCTCGCTCA	6480
1886	CCCAGCCG	CICCACAGCI	CCITCATCIC	CIGGAGACAA	ACICIGICCG	CCCICGCICA	0-200
1887	TTCACTTGTT	CGTCCTAAAT	CCGAGATGAT	AAAGCTTCGA	GGGGGGTTG	GGGTTCCATC	6540

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1888							
1889	AGGGCTGCCC	TTCCGCCGGG	CAGCCTGGGC	CACATCTGCC	CTTGGCCCCC	TCAGGACTCA	6600
1890							
1891 1892	CTCTGACTGG	AGGCCCTGCA	CTGACTGACG	CCAGGGTGCC	CAGCCCAGGG	TCTCTGGCGC	6660
1893	CATCCAGCTG	CACTGGGTTT	GGGTGCTGGT	CCTGCCCCCA	AGCTGCCCGG	ACACCACAGG	6720
1894							
1895	CAGCCGGGGC	TGCCCACTGG	CCTCGGTCAG	GGTGAGCCCC	AGCTGCCCCC	GCTCAGGGCT	6780
1896 1897	TGCCCCGACA	ATGACCCCAT	CCTCAGGACG	СУССССССТТ	СССТТССТСС	ССУСТСТССУ	6840
1898	Ideceedhen	HIGHCCCCHI	CCTCAGGACG	CACCCCCII	0001100100	GCAGIGICCA	0010
1899	GCCCCACCCG	AGATCGGGGG	AAGCCCTATT	TCTTGACAAC	TCCAGTCCCT	GGGGGAGGG	6900
1900							
1901 1902	GCCTCAGACT	GAGTGGTGAG	TGTTCCCAAG	TCCAGGAGGT	GGTGGAGGGT	CCTGGCGGAT	6960
1902	CCAGAGTTGA	CAGTGAGGGC	TTCCTGGGCC	CCATGCGCCT	GGCAGTGGCA	GCAGGGAAGA	7020
1904							
1905	GGAAGCACCA	TTTCAGGGGT	GGGGGATGCC	AGAGGCGCTC	CCCACCCCGT	CTTCGCCGGG	7080
1906							=
1907 1908	TGGTGACCCC	GGGGGAGCCC	CGCTGGTCGT	GGAGGGTGCT	GGGGGCTGAC	TAGCAACCCC	7140
1909	TCCCCCCCG	TTGGAACTCA	CTTTTCTCCC	GTCTTGACCG	CGTCCAGCCT	TGAATGAGAA	7200
1910							
1911	CAAAGTCCTT	GTGCTGGACA	CCGACTACAA	AAAGTACCTG	CTCTTCTGCA	TGGAAAACAG	7260
1912		~-~~-		~~~~~~~		~~~~~~~	=
1913 1914	TGCTGAGCCC	GAGCAAAGCC	TGGCCTGCCA	GTGCCTGGGT	GGGTGCCAAC	CCTGGCTGCC	7320
1914	CAGGGAGACC	AGCTGCGTGG	TCCTTGCTGC	AACAGGGGGT	GGGGGGTGGG	AGCTTGATCC	7380
1916							,
1917	CCAGGAGGAG	GAGGGGTGGG	GGGTCCCTGA	GTCCCGCCAG	GAGAGAGTGG	TCGCATACCG	7440
1918	~~~~~~				~~~~~~	~-~-	
1919 1920	GGAGCCAGTC	TGCTGTGGGC	CTGTGGGTGG	CTGGGGACGG	GGGCCAGACA	CACAGGCCGG	7500
1921	GAGACGGGTG	GGCTGCAGAA	CTGTGACTGG	TGTGACCGTC	GCGATGGGGC	CGGTGGTCAC	7560
1922							
1923	TGAATCTAAC	AGCCTTTGTT	ACCGGGGAGT	TTCAATTATT	TCCCAAAATA	AGAACTCAGG	7620
1924	ma	mammaa a am	> = C > C > = C C = C	G3333G333E	ассъ сспоъс	a mmmmamama	7600
1925 1926	TACAAAGCCA	TCTTTCAACT	ATCACATCCT	GAAAACAAAT	GGCAGGTGAC	ATTITCTGTG	7680
1927	CCGTAGCAGT	CCCACTGGGC	ATTTTCAGGG	CCCCTGTGCC	AGGGGGGCGC	GGGCATCGGC	7740
1928							
1929	GAGTGGAGGC	TCCTGGCTGT	GTCAGCCGGC	CCAGGGGGAG	GAAGGGACCC	GGACAGCCAG	7800
1930		a. aaammaa	~~~~~~	maa. a. aaa.	amaar amaaa	amaaaa aa a	7060
1931 1932	AGGTGGGGGG	CAGGCTTTCC	CCCTGTGACC	TGCAGACCCA	CTGCACTGCC	CTGGGAGGAA	7860
1933	GGGAGGGGAA	CTAGGCCAAG	GGGGAAGGGC	AGGTGCTCTG	GAGGGCAAGG	GCAGACCTGC	7920
1934							
1935	AGACCACCCT	GGGGAGCAGG	GACTGACCCC	CGTCCCTGCC	CCATAGTCAG	GACCCCGGAG	7980
1936	amaan an na	3 00 00 0 m 0 0 5	0333mmcc.c.c	3330000000	3.00000macc	03 m003 03 m0	0040
1937 1938	GTGGACAACG	AGGCCCTGGA	GAAATTCGAC	AAAGCCCTCA	AGGCCCTGCC	CATGCACATC	8040
1730							

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1939	CGGCTTGCCT	TCAACCCGAC	CCAGCTGGAG	GGTGAGCACC	CAGGCCCCGC	CCTTCCCCAG	8100
1940							
1941	GGCAGGAGCC	ACCCGGCCCC	GGGACGACCT	CCTCCCATGG	TGACCCCCAG	CTCCCCAGGC	8160
1942							
1943	CTCCCAGGAG	GAAGGGGTGG	GGTGCAGCAC	CCCGTGGGGG	CCCCCTCCCC	ACCCCCTGCC	8220
1944						•	
1945	AGGCCTCTCT	TCCCGAGGTG	TCCAGTCCCA	TCCTGACCCC	CCCATGACTC	TCCCTCCCCC	8280
1946		~~~~				~~~~~~	
1947	ACAGGGCAGT	GCCACGTCTA	GGTGAGCCCC	TGCCGGTGCC	TCTGGGGTAA	GCTGCCTGCC	8340
1948	amaaaaaa aa	таатаааа а	1 C1 C1 ECCCC	тъ сососитет	таатаааааа	magan agaan	0.400
1949	CTGCCCCACG	TCCTGGGCAC	ACACATGGGG	TAGGGGGTCT	TGGTGGGGCC	TGGGACCCCA	8400
1950	armar agaaa	magaamaaaa	aamamaa aa a	maaamaaaaa	amagaamaaa	maamaaaaa a	0.4.5.0
1951	CATCAGGCCC	TGGGGTCCCC	CCTGTGAGAA	TGGCTGGAAG	CTGGGGTCCC	TCCTGGCGAC	8460
1952	maar ar aama	аатааааааа	magaz amamm	CDCCCDCA CC	тататаатаа	CCECT CT CT C	0500
1953	TGCAGAGCTG	GCTGGCCGCG	TGCCACTCTT	GTGGGTGACC	TGTGTCCTGG	CCTCACACAC	8520
1954	man aamaama	CA COMOCHINO	Cr CCr Cr CCT	3 3 CCCCM3 3 CF	G3.GGG3.G3.3.E	CCTT CCTT AC	0.500
1955 1956	TGACCTCCTC	CAGCICCITC	CAGCAGAGCT	AAGGCTAAGT	GAGCCAGAAT	GGTACCTAAG	8580
1956	CCC2 CCCT2 C	CCCTCCTTTCT		GGCTGTCCTG	CARCOACOAC	aan maan an a	0640
1958	GGGAGGCIAG	CGGICCIICI	CCCGAGGAGG	GGCIGICCIG	GAACCACCAG	CCAIGGAGAG	8640
1959	CCTCCCAACC	СТСТСССХСС	שרכים בים אינים איני	ATCACAGGGG	CCCCCCATCT	מרא יייייירי א מר	8700
1960	GCIGGCAAGG	GICIGGCAGG	IGCCCCAGGA	ATCACAGGGG	GGCCCCAIGI	CCATTICAGG	8700
1961	GCCCGGGAGC	CTTCC7 CTCC	тстсссслсл	GACGACGTCA	CCACCGCCCC	CCCCCCATCA	8760
1962	GCCCGGGAGC	CIIGGACICC	TCTGGGGACA	GACGACGICA	CCACCGCCCC	CCCCCATCA	8700
1963	CCCCACTAC	אמפפאפפאפ	מא כיתמ כי א מית כי	ACCCTTCCTG	CCACCCACCC	СССТССЛССС	8820
1964	GGGGGACIAG	ANGGGACCAG	GACIGCAGIC	ACCCITCCIG	GGACCCAGGC	CCCTCCAGGC	0020
1965	СССТССТССС	CCTCCTCCTC	тесеслестт	CTCCTTCACC	א א דא א א מכיכי <i>א</i>	ጥ እ እ	8880
1966	cccrccraaa	GCICCIGCIC	IGGGCAGCII	CICCIICACC	AAIAAAGCA	TARACCIGIG	0000
1967	<u>כידכידכיכיכידידכ</u>	ጥር አርጥር ጥጥጥር	СТССАССАСС	GGCAGGGGGT	CCACAACTCC	TCCCCACCCA	8940
1968	CICICCCIIC	IGAGICIIIG	CIGOACOACO	GGCAGGGGG	GGAGAAGIGG	LOCOGOGOGA	0740
1969	GTCTGGCTCA	GAGGATGACA	ссессстес	GATCCAGGGC	СТСТССАТСА	СУСТСТТСТС	9000
1970	01010001011	000	000000000	011100110000	010100111011	001011010	3000
1971	ACAACTGGGG	GCCCACACAC	ATCACTGCGG	CTCTTTGAAA	СТТТСАССАА	CCAGGGAGGG	9060
1972		3000110110110		01011101111	011101100111	001100011000	2000
1973	ACTCGGCAGA	GACATCTGCC	AGTTCACTTG	GAGTGTTCAG	TCAACACCCA	AACTCGACAA	9120
1974							
1975	AGGACAGAAA	GTGGAAAATG	GCTGTCTCTT	AGTCTAATAA	ATATTGATAT	GAAACTCAAG	9180
1976							
1977	TTGCTCATGG	ATCAATATGC	CTTTATGATC	CAGCCAGCCA	CTACTGTCGT	ATCAACTCAT	9240
1978							
1979	GTACCCAAAC	GCACTGATCT	GTCTGGCTAA	TGATGAGAGA	TTCCCAGTAG	AGAGCTGGCA	9300
1980							
1981	AGAGGTCACA	GTGAGAACTG	TCTGCACACA	CAGCAGAGTC	CACCAGTCAT	CCTAAGGAGA	9360
1982							
1983	TCAGTCCTGG	TGTTCATTGG	AGGACTGATG	TTGAAGCTGA	AACTCCAATG	CTTTGGCCAC	9420
1984							
1985	CTGATGTGAA	GAGCTGACTC	ATTTGAAAAG	ACCCTGATGC	TGGGAAAGAT	TGAGGGCAGG	9480
1986							
1987	AGGAGAAGGG	GACGACAGAG	GATGAGATGG	TTGGATGGCA	TCACCAACAC	AATGGACATG	9540
1988							
1989	GGTTTGGGTG	GACTCCAGGA	GTTGGTGATG	GACAGGGAGG	CCTGGCGTGC	TACGGAAGCG	9600

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1990		
1991	GTTTATGGGG TCACAAAGAC TGAGTGACTG AACTGAGCTG AACTGAATGG AAATGAGGTA	9660
1992		
1993	TACAGCAAAG TGGGGATTTT TTAGATAATA AGAATATACA CATAACATAG TGTATACTCA	9720
1994 1995	TATTTTTATG CATACCTGAA TGCTCAGTCA CTCAGTCGTA TCTGACTCTG TGACCTATGG	9780
1996	IMITITATO CATACCIONA IOCICACIONA CICACIONA ICIONCICIO IGACCINIGO	3700
1997	ACCGTAGCCT TCCAGGTTTC TTCTGTCCAC AGAATTCTCC AAGGCAAGAA TACTGGAGTG	9840
1998		
1999	GGTAGCCATT TCCTCCTCCA GGGGATCCTC CCGACCCAGG GATTGAACCG GCATCTCCTG	9900
2000 2001	TATTGGCAGG TGGATTCTTT ACCACTGTGC CACCAGGGAA GCCCGTGTTA CTCTCTATGT	9960
2002	TATIOGCAGG IGGATICTIT ACCACIGIGC CACCAGGGAA GCCCGIGITA CICICIAIGI	3360
2003	CCCACTTAAT TACCAAAGCT GCTCCAAGAA AAAGCCCCTG TGCCCTCTGA GCTTCCCGGC	10020
2004		
2005	CTGCAGAGGG TGGTGGGGGT AGACTGTGAC CTGGGAACAC CCTCCCGCTT CAGGACTCCC	10080
2006 2007	CCCCCA COMC. A CCCA CA CMCCA CA CACA CA CACA CACA	10140
2007	GGGCCACGTG ACCCACAGTC CTGCAGACAG CCGGGTAGCT CTGCTCTTCA AGGCTCATTA	10140
2009	TCTTTAAAAA AAACTGAGGT CTATTTTGTG ACTTCGCTGC CGTAACTTCT GAACATCCAG	10200
2010		
2011	TGCGATGGAC AGGACCTCCT CCCCAGGCCT CAGGGGCTTC AGGGAGCCAG CCTTCACCTA	10260
2012		
2013 2014	TGAGTCACCA GACACTCGGG GGTGGCCCCG CCTTCAGGGT GCTCACAGTC TTCCCATCGT	10320
2015	CCTGATCAAA GAGCAAGACC AATGACTTCT TAGGAGCAAG CAGACACCCA CAGGACACTG	10380
2016		10300
2017	AGGTTCACCA GAGCTGAGCT GTCCTTTTGA ACCTAAAGAC ACACAGCTCT CGAAGGTTTT	10440
2018		
2019	CTCTTTAATC TGGATTTAAG GCCTACTTGC CCCTCAAGAG GGAAGACAGT CCTGCATGTC	10500
2020 2021		
2022	CCCAGGACAG CCACTCGGTG GCATCCGAGG CCACTTAGTA TTATCTGACC GCACCCTGGA	10560
2023		
2024	ATTAATCGGT CCAAACTGGA CAAAAACCTT GGTGGGAAGT TTCATCCCAG AGGCCTCAAĆ	10620
2025		
2026 2027	CATCCTGCTT TGACCACCCT GCATCTTTTT TTCTTTTATG TGTATGCATG TATATATATA	10680
2027	TATATATTT TTTTTTTTC ATTTTTTGGC TGTGCTGGCT GTTCGTTGCA GTTCGGTGCG	10740
2029		10,10
2030	CAGGCTTCTC TCTAGTTTCT CTCTAGTCTT CTCTTATCAC AGAGCAGTCT CTAGACGATC	10800
2031		
2032	GACGCGT	10807
2033 2034	(2) INFORMATION FOR SEQ ID NO:8:	
2034	(2) INIONATION FOR DEQ ID NO.0.	
2036	(i) SEQUENCE CHARACTERISTICS:	
2037	(A) LENGTH: 47 base pairs	
2038	(B) TYPE: nucleic acid	
2039	(C) STRANDEDNESS: single	
2040	(D) TOPOLOGY: linear	

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2041		
2042		
2043		
2044	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
2045		
2046	AATTCCGATC GACGCGTCGA CGATATACTC TAGACGATCG ACGCGTA	47
2047	(0) 5	
2048	(2) INFORMATION FOR SEQ ID NO:9:	
2049	(:) ODOLITINOD GWADAGEDDIGE	
2050 2051	(i) SEQUENCE CHARACTERISTICS:	
2051	(A) LENGTH: 24 base pairs (B) TYPE: nucleic acid	
2052	(C) STRANDEDNESS: single	
2054	(D) TOPOLOGY: linear	
2055	(b) TOPOLOGI: Timear	
2056		
2057	(vii) IMMEDIATE SOURCE:	
2058	(B) CLONE: BLGAMP3	
2059	(b) Chorn. Bloames	
2060		
2061	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
2062	(MI) BEGOLMED BESCHILLION. BEG IS NO. J.	
2063	TGGATCCCCT GCCGGTGCCT CTGG	24
2064		
2065		
2066	(2) INFORMATION FOR SEQ ID NO:10:	
2067		
2068	(i) SEQUENCE CHARACTERISTICS:	
2069	(A) LENGTH: 24 base pairs	
2070	(B) TYPE: nucleic acid	
2071	(C) STRANDEDNESS: single	
2072	(D) TOPOLOGY: linear	
2073		
2074		
2075	(vii) IMMEDIATE SOURCE:	
2076	(B) CLONE: BLGAMP4	
2077		
2078		
2079	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
2080		
2081	AACGCGTCAT CCTCTGTGAG CCAG	24
2082	(2)	
2083	(2) INFORMATION FOR SEQ ID NO:11:	
2084	(i) anathian attana ampriantas	
2085	(i) SEQUENCE CHARACTERISTICS:	
2086 2087	(A) LENGTH: 10 base pairs	
2087	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
2088	(D) TOPOLOGY: linear	
2099	(D) TOPOHOGI. IIIIEAI	
2090		

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2092	(vii)	IMMEDIATE SOURCE:	
2093		(B) CLONE: ZC6839	
2094			
2095		·	
2096	(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:11:	
2097			
2098	ACTACGTAGT	r	10
2099			
2100	(2) INFORM	MATION FOR SEQ ID NO:12:	
2101			
2102	(i) S	SEQUENCE CHARACTERISTICS:	
2103		(A) LENGTH: 42 base pairs	
2104		(B) TYPE: nucleic acid	
2105		(C) STRANDEDNESS: single	
2106		(D) TOPOLOGY: linear	
2107			
2108			
2109	(vii)	IMMEDIATE SOURCE:	
2110	, ,	(B) CLONE: ZC6632	
2111			
2112			
2113	(xi) S	SEQUENCE DESCRIPTION: SEQ ID NO:12:	
2114	, ,	~	
2115	CGACGCGGAT	I CCTACGTACC TGCAGCCATG TTTTCCATGA GG	42
2116			
2117	(2) INFORM	MATION FOR SEQ ID NO:13:	
2118		~	
2119	(i) S	SEQUENCE CHARACTERISTICS:	
2120		(A) LENGTH: 21 base pairs	
2121		(B) TYPE: nucleic acid	
2122		(C) STRANDEDNESS: single	
2123		(D) TOPOLOGY: linear	
2124		(-,	
2125			
2126	(vii)	IMMEDIATE SOURCE:	
2127	(, -	(B) CLONE: ZC6627	
2128		• • • • • • • • • • • • • • • • • • • •	
2129			
2130	(xi) 8	SEQUENCE DESCRIPTION: SEQ ID NO:13:	
2131	(, -		
2132	AGGGCTTCGC	G CAAGCTTCAG G	21
2133			
2134	(2) INFORM	MATION FOR SEQ ID NO:14:	
2135	.=,	· · · · · · · · · · · · · · · · · · ·	
2136	(i) 9	SEQUENCE CHARACTERISTICS:	
2137	\-, ·	(A) LENGTH: 24 base pairs	
2138		(B) TYPE: nucleic acid	•
2139		(C) STRANDEDNESS: single	
2140		(D) TOPOLOGY: linear	
2141		,	
2142			
			

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2143 2144 2145 2146 2147 2148 2149	(vii) IMMEDIATE SOURCE: (B) CLONE: ZC6521 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14: GCCAAAGACT TACTTCCCTC TAGA	24
2150		
2151	(2) THEODMAND DOD GEO TO NO 15	
2152 2153	(2) INFORMATION FOR SEQ ID NO:15:	
2154	(i) SEQUENCE CHARACTERISTICS:	
2155	(A) LENGTH: 30 base pairs	
2156	(B) TYPE: nucleic acid	
2157	(C) STRANDEDNESS: single	
2158	(D) TOPOLOGY: linear	
2159		
2160		
2161	(vii) IMMEDIATE SOURCE:	
2162	(B) CLONE: ZC6520	
2163		
2164	(wi) GEOVERNOE DEGODEDATON GROUND 15	
2165 2166	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
2166	GCATGAACGT CGCGTGGTGG TTGTGCTACC	30
2168	GCATGAACGT CGCGTGGTGG TTGTGCTACC	30
2169	(2) INFORMATION FOR SEQ ID NO:16:	
2170	(a) annotable for bag ab notion	
2171	(i) SEQUENCE CHARACTERISTICS:	
2172	(A) LENGTH: 30 base pairs	
2173	(B) TYPE: nucleic acid	
2174	(C) STRANDEDNESS: single	
2175	(D) TOPOLOGY: linear	
2176		
2177	() ()	
2178	(vii) IMMEDIATE SOURCE:	
2179 2180	(B) CLONE: ZC6519	
2180		
2182	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
2183	(MI) DESCRICE DESCRIPTION. DES ES MOLEO.	
2184	ACCACGCGAC GTTCATGCTC TAAAACCGTT	30
2185		
2186	(2) INFORMATION FOR SEQ ID NO:17:	
2187		
2188	(i) SEQUENCE CHARACTERISTICS:	
2189	(A) LENGTH: 36 base pairs	
2190	(B) TYPE: nucleic acid	
2191	(C) STRANDEDNESS: single	
2192 2193	(D) TOPOLOGY: linear	
4173		

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2194			
2195	(vii)	IMMEDIATE SOURCE:	
2196		(B) CLONE: ZC6518	
2197			
2198			
2199	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:17:	
2200		•	
2201	GCTGCGGG.	AT CCTACGTACT AGGGGGACAG GGAAGG	36
2202			
2203	(2) INFO	RMATION FOR SEQ ID NO:18:	
2204			
2205	(i)	SEQUENCE CHARACTERISTICS:	
2206		(A) LENGTH: 45 base pairs	
2207		(B) TYPE: nucleic acid	
2208		(C) STRANDEDNESS: single	
2209		(D) TOPOLOGY: linear	
2210			
2211	12 11	TIMEDIA DE COUDCE	
2212	(V11)	IMMEDIATE SOURCE:	
2213		(B) CLONE: ZC6629	
2214			
2215 2216	()	GEOTIENGE DEGGETOW GEO. ID NO. 10	
2216	(XI)	SEQUENCE DESCRIPTION: SEQ ID NO:18:	
2217	CCACCCCA	AT TCTACGTACC TGCAGCCATG AAAAGGATGG TTTCT	45
2218	CGACGCGA	AT TOTACGTACC TGCAGCCATG AAAAGGATGG TITCT	45
2219	(2) TNEO	RMATION FOR SEQ ID NO:19:	
2221	(2) INFO	MARION FOR SEQ ID NO.19.	
2222	(5)	SEQUENCE CHARACTERISTICS:	
2223	(1)	(A) LENGTH: 45 base pairs	
2224		(B) TYPE: nucleic acid	
2225		(C) STRANDEDNESS: single	
2226		(D) TOPOLOGY: linear	
2227		(5) 101010011 111001	
2228			
2229	(vii)	IMMEDIATE SOURCE:	
2230	, -,	(B) CLONE: ZC6630	
2231			
2232			
2233	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:19:	
2234			
2235	CGACGCGA	AT TCTACGTACC TGCAGCCATG AAACATCTAT TATTG	45
2236			
2237			
2238	(2) INFO	RMATION FOR SEQ ID NO:20:	
2239			
2240	(i)	SEQUENCE CHARACTERISTICS:	
2241		(A) LENGTH: 21 base pairs	
2242		(B) TYPE: nucleic acid	
2243		(C) STRANDEDNESS: single	
2244		(D) TOPOLOGY: linear	

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2245 2246 2247 2248	(vii) IMMEDIATE SOURCE: (B) CLONE: ZC6625	
2249 2250 2251	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
2252	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
2253 2254	GTGAGATTTT CAGATCTTGT C	21
2255	(2) INFORMATION FOR SEQ ID NO:21:	
2256 2257 2258 2259 2260 2261 2262	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
2263	() TAMED TAME COUNCE	
2264 2265 2266	(vii) IMMEDIATE SOURCE: (B) CLONE: ZC6626	
2267 2268 2269	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
2270	AAGAATTACT GTGGCCTACC A	21
2271 2272 2273	(2) INFORMATION FOR SEQ ID NO:22:	
2274 2275 2276 2277 2278 2279 2280	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
2281 2282 2283 2284 2285	(vii) IMMEDIATE SOURCE: (B) CLONE: ZC6624	
2286	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
2287 2288 2289	GCTGCGGAAT TCTACGTACT ATTGCTGTGG GAA	33
2289 2290 2291	(2) INFORMATION FOR SEQ ID NO:23:	
2291 2292 2293 2294 2295	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 45 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

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DATE: 03/23/94 TIME: 15:05:13

2298 2299 (vii) IMMEDIATE SOURCE: 2300 (B) CLONE: ZC6514 2301 2302 2303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: 2304 2305 CGACGCGGAT CCTACGTACC TGCAGCCATG AGTTGGTCCT TGCAC 2306 2307 (2) INFORMATION FOR SEQ ID NO:24: 2308 2309 (i) SEQUENCE CHARACTERISTICS: 2310 (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: Zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2322 2333 (xi) SEQUENCE CHARACTERISTICS: 2334 (xi) IMMEDIATE SOURCE: 2335 (B) TYPE: nucleic acid 2336 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: Zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 242 24341 (2) INFORMATION FOR SEQ ID NO:26: 2344 2345 (A) LENGTH: 22 base pairs 2346 (B) TYPE: nucleic acid 2347 (C) INFORMATION FOR SEQ ID NO:26: 2344 (I) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs 2346 (B) TYPE: nucleic acid	2296 2297	(D) TOPOLOGY: linear	
2302 2303 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: 2304 2305 CGACGCGGAT CCTACGTACC TGCAGCCATG AGTTGGTCCT TGCAC 2306 2307 (2) INFORMATION FOR SEQ ID NO:24: 2308 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2321 2322 GTCTCTGGTA GCAACATACT A 21 2322 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid 2327 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2366 2377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2389 (G) TYPE: nucleic acid 2391 2392 2393 2394 (vii) IMMEDIATE SOURCE: 2395 2396 (S) CLONE: zc6516 2367 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2389 2399 (S) CLONE: zc6516 2340 (G) CLONE: zc6516 2341 (2) INFORMATION FOR SEQ ID NO:26: 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 (4) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs	2299 2300	• •	
2305 CGACGCGGAT CCTACGTACC TGCAGCCATG AGTTGGTCCT TGCAC 45 2306 (2) INFORMATION FOR SEQ ID NO:24: 2307 (2) INFORMATION FOR SEQ ID NO:24: 2310 (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 (B) CLONE: zc6517 2318 2319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 GTCTCTGGTA GCAACATACT A 21 2322 GTCTCTGGTA GCAACATACT A 21 2323 (2) INFORMATION FOR SEQ ID NO:25: 2326 (A) LENGTH: 22 base pairs 2327 (I) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 (Vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 (B) CLONE: zc6516 2337 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 (GCTTCTGG CCTACTAGT AG 22 2341 (2) INFORMATION FOR SEQ ID NO:26: 2343 (i) SEQUENCE CHARACTERISTICS: 2344 (2) INFORMATION FOR SEQ ID NO:26: 2345 (A) LENGTH: 22 base pairs	2302	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
2306 2307 (2) INFORMATION FOR SEQ ID NO:24: 2308 2309 (i) SEQUENCE CHARACTERISTICS: 2310 (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2330 (G) STRANDEDNESS: single 2331 (Vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs		CGACGCGGAT CCTACGTACC TGCAGCCATG AGTTGGTCCT TGCAC	45
2308 2309 (i) SEQUENCE CHARACTERISTICS: 2310 (A) LENOTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs	2306		
2309 (i) SEQUENCE CHARACTERISTICS: 2310 (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2341 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(2) INFORMATION FOR SEQ ID NO:24:	
2310 (A) LENGTH: 21 base pairs 2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2334 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2341 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2311 (B) TYPE: nucleic acid 2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2341 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2344 (i) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2345 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2312 (C) STRANDEDNESS: single 2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTCTAG CCCTACTAGT AG 22 2341 2341 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		<u>-</u>	
2313 (D) TOPOLOGY: linear 2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2314 2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs			
2315 2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(b) TOPOLOGI: Tillear	
2316 (vii) IMMEDIATE SOURCE: 2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2317 (B) CLONE: zc6517 2318 2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(vii) IMMEDIATE SOURCE:	
2319 2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		, , , , , , , , , , , , , , , , , , , ,	
2320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: 2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs	2318		
2321 2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs	2319		
2322 GTCTCTGGTA GCAACATACT A 21 2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs	2320	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
2323 2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2324 2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		GTCTCTGGTA GCAACATACT A	21
2325 (2) INFORMATION FOR SEQ ID NO:25: 2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2326 2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(0)	
2327 (i) SEQUENCE CHARACTERISTICS: 2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(2) INFORMATION FOR SEQ ID NO:25:	
2328 (A) LENGTH: 22 base pairs 2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(i) CECHENGE GUADAGEDIGE	
2329 (B) TYPE: nucleic acid 2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2330 (C) STRANDEDNESS: single 2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2331 (D) TOPOLOGY: linear 2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2332 2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2333 2334 (vii) IMMEDIATE SOURCE: 2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		_,	
2335 (B) CLONE: zc6516 2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2336 2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs	2334	(vii) IMMEDIATE SOURCE:	
2337 2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(B) CLONE: zc6516	
2338 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: 2339 2340 GGGTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2339 2340 GGGTTTCTAG CCCTACTAGT AG 22 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs			
2340 GGGTTTCTAG CCCTACTAGT AG 2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
2341 2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		GGGTTTTGTT3 G GGGTT3 GTT3 GTT 3 G	
2342 (2) INFORMATION FOR SEQ ID NO:26: 2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		GGGTTTCTAG CCCTACTAGT AG	22
2343 2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(2) INFORMATION FOR SEC ID NO.26.	
2344 (i) SEQUENCE CHARACTERISTICS: 2345 (A) LENGTH: 22 base pairs		(2) INFORMATION FOR SEQ ID NO:20:	
2345 (A) LENGTH: 22 base pairs		(i) SEQUENCE CHARACTERISTICS:	
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:05:19

2347	(C) STRANDEDNESS: single	
2348	(D) TOPOLOGY: linear	
2349		
2350		
2351	(vii) IMMEDIATE SOURCE:	
2352	(B) CLONE: zc6515	
2353		
2354		
2355	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
2356		
2357	GGGTTTCTAG CCCTACTAGT AG	22
2358		
2359		
2360	(2) INFORMATION FOR SEQ ID NO:27:	
2361		
2362	(i) SEQUENCE CHARACTERISTICS:	
2363	(A) LENGTH: 47 base pairs	
2364	(B) TYPE: nucleic acid	
2365	(C) STRANDEDNESS: single	
2366	(D) TOPOLOGY: linear	
2367		
2368		
2369		
2370	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
2371		
2372	AAGCTACGCG TCGATCGTCT AGAGTATATC GTCGACGCGT CGATCGG	47
2373		
2374		

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:05:24

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Line Error

Original Text

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:05:24

INPUT SET: S2548.raw

APPLICATION NUMBER FILING DATE PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/206,176

DATE: 03/23/94 TIME: 15:05:25

INPUT SET: S2548.raw

Line

Original Text

Corrected Text